

309 MLFGPGAVSEVNNGTSSRAGCIWLLPLVLLHLLKF 344

Db

RESULT 5

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CEPU_CHICK
ID CEPU_CHICK STANDARD; PRT; 353 AA.
AC Q90773;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE CEPU-1 protein precursor.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Gallus gallus (Chicken).
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=96370549; PubMed=8774445;
RA Spaltmann F., Brummendorf T.;
RT "CEPU-1, a novel immunoglobulin superfamily molecule, is expressed by
  developing cerebellar Purkinje cells.";
RL J. Neurosci. 16:1770-1779(1996).
CC -!- FUNCTION: It may be a cellular address molecule specific to
  Purkinje cells. It may represent a receptor or a subunit of a
  receptor complex.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- ALTERNATIVE PRODUCTS:
  Event=Alternative splicing; Named isoforms=2;
  Name=1; Synonyms=Minor;
  IsoId=Q90773-1; Sequence=Displayed;
  Name=2; Synonyms=Major;
  IsoId=Q90773-2; Sequence=VSP_002607;
CC -!- TISSUE SPECIFICITY: Found on the dendrites, somata and axons of
  developing Purkinje cells. Undetectable on other neurons like
  Golgi or granule cells.
CC -!- DEVELOPMENTAL STAGE: Expressed by developing cerebellar Purkinje
  cells. Expression coincides with the growth of the dendritic tree,
  after Purkinje cells have finished their migration from the
  ventricular zone (from E15 until E21). Expressed in the adult.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
  family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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EMBL; Z72497; CAA96578.1; -.
InterPro; IPR007110; IG-like.
InterPro; IPR003598; IG_c2.
Pfam; PF00047; IG_3.
SMART; SM00408; IGC2; 2.
PROSITE; PS00835; IG_LIKE; 3.
KW Alternative splicing; Cell adhesion; Glycoprotein; GPI-anchor;
  Immunoglobulin domain; Lipoprotein; Repeat; Signal.
FT SIGNAL 1 28
FT CHAIN 29 330
FT PROPEP 331 353
FT DOMAIN 37 124
FT DOMAIN 134 216
FT DOMAIN 220 314
FT DISULFID 55 113
FT DISULFID 155 199
FT DISULFID 241 293
FT CARBOHYD 42 42
FT CARBOHYD 68 68
FT CARBOHYD 150 150
  
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FT CARBOHYD 282 282 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 290 290 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 303 303 N-linked (GlcNAc...) (Potential).
FT LIPID 330 330 GPI-anchor amidated serine (Potential).
FT VARSPLIC 310 320 Missing (in isoform 2).
FT SEQUENCE 353 AA; 38736 MW; 2550C48591EBBA6 CRC64;
  Query Match 81.8%; Score 1477.5; DB 1; Length 353;
  Best Local Similarity 78.6%; Pred. No. 2e-109;
  Matches 276; Conservative 32; Mismatches 32; Indels 11; Gaps 1;
QY 5 QPKHNSISWAFITGLAALCLFQGVVRSRGDATTTPKAMDNVTVRGEGSATLRCTIDNRVT 64
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 QAKQHQPVSWSWIFAGMAALLLFQGVVRSRGDATTTPKAMDNVTVRGEGSATLRCSVDNRVT 62
QY 65 RVAMLNRSITLYAGNDKWCCLDRVLLSNTQYISIEIQNVYDVGDEGPTCSVQTDNHPK 124
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 RVAMLNRSITLYAGNDKWCCLDRVLLSNTQYISIEIQNVYDVGDEGPTCSVQTDNHPK 122
QY 125 TSVHVLIVQSPKIVEISSDISINEGNISITCIATGHPETVTVRRHISPKAVGVSEDE 184
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
123 TSVHVLIVQSPKIVETSSDISINEGNISITCIATGHPETVTVRRHISPKAVGVSEDE 182
QY 185 YLEIQGITREOSGDYECASNDVAAPVVRVKVTWNPYIYSEAKGTGVPVGOKGTLOCE 244
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
183 YLEITGITREOSGEYECASNDVAAPVVRVKVTWNPYIYSEAKGTGVPVGOKGILMCE 242
QY 245 ASAVPSAEFQWKDKRLIEGKGVKVENRPLSKLIFPNVSEHDYNYTVCASNKLGH 304
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
243 ASAVPSAEFQWKDKRLAEQKGLKVENKAPFSLTFENVSEQDYGYNYTVCASNQLGNT 302
QY 305 NASIMLP-----GPCAVSEVNGTSRRAGCIWLLPLVLLHLLKF 344
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
303 NASIMLYEETTTALTTPKPGAVHGDGNSGAWRRGSCAWLLALPLAQLARQF 353
RESULT 6
O57596 PRELIMINARY; PRT; 313 AA.
AC O57596;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Neural secreted glycoprotein (CEPU-Se alpha 2 isoform).
GN Name=CEPU; Synonyms=CEPU-Se;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99347334; PubMed=10420985;
RA Kim D.S., Rhew T.H., Moss D.J., Kim J.Y.;
RT "cDNA cloning of the CEPU, a secreted type of neural glycoprotein
  belonging to the immunoglobulin-like oploid binding cell adhesion
  molecule (OBCAM) subfamily.";
RL Mol. Cells 9:270-276(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX Kim D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225897; CAA12649.1; -.
DR EMBL; AF292935; AAG01878.1; -.
DR HSSP; Q9UQH9; 1DJS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
  
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FT DISULFID 157 201 Potential.
FT DISULFID 243 295 Potential.
FT CARBOHYD 44 44 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 70 70 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 152 152 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 284 284 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 305 305 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 321 321 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 321 321 GPI-anchor amidated asparagine
FT LIPID (Potential).
FT CONFLICT 75 75 L -> P (in Ref. 1).
FT CONFLICT 92 92 S -> Q (in Ref. 1).
FT CONFLICT 119 119 T -> I (in Ref. 1).
FT CONFLICT 187 187 E -> Q (in Ref. 1).
FT CONFLICT 213 213 R -> P (in Ref. 1).
FT CONFLICT 225 225 I -> F (in Ref. 1).
SQ SEQUENCE 344 AA; 37984 MW; C865BBA52C148554 CRC64;

Query Match 91.2%; Score 1647.5; DB/1; Length 344;
Best Local Similarity 93.5%; Pred. No. 5.3e-123;
Matches 314; Conservative 8; Mismatches 11; Indels 3; Gaps 1;

QY 12 ISWALFTGLAALCLF---QGVPRSGDATFPKAMDNVTVRQGESATLRCCTIDNRVTRVAV 68
Db 9 LPWKCLVWVSLRLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCCTIDNRVTRVAV 68

QY 69 LNRSTLYAGNDKWCLDRPVLLSNTQYISIEIQNVVDYDGGPYTCSVQTDNHPKTSRV 128
Db 69 LNRSTLYAGNDKWCLDRPVLLSNTQYISIEIQNVVDYDGGPYTCSVQTDNHPKTSRV 128

QY 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFVSEDEYLEI 188
Db 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFVSEDEYLEI 188

QY 189 QGITREQSDYECSSASNDVAAPVVRVKVTNNYPPISEAKGTGVPVQKGLQCEASAV 248
Db 189 QGITREQSDYECSSASNDVAAPVVRVKVTNNYPPISEAKGTGVPVQKGLQCEASAV 248

QY 249 PSAEFQWKDKRLLEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVSNKLGHTNASI 308
Db 249 PSAEFQWKDKRLLEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVSNKLGHTNASI 308

QY 309 MLFGGAVSEVNGTSRRAGCVLLPLLVHLLKLF 344
Db 309 MLFGGAVSEVNGTSRRAGCVLLPLLVHLLKLF 344
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RESULT 4
NTRI RAT STANDARD; PRT; 344 AA.
AC Q62718;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neurotrophin precursor (GP65).
GN Name=Nt;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 217-229.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=95198094; PubMed=7891157;
RA Struyk A.F., Canoll P.D., Wolfgang M.J., Rosen C.L., D'Eustachio P.,
RA Salzer J.L.;
RT "Cloning of neurotrophin defines a new subfamily of differentially
RT expressed neural cell adhesion molecules.";
RL J. Neurosci. 15:2141-2156(1995)
CC -!- FUNCTION: Neural cell adhesion molecule.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: Central nervous system.
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CC -!- DEVELOPMENTAL STAGE: Expressed at high levels in several
CC developing projection systems: in neurons of the thalamus,
CC subplate, and lower cortical laminae in the forebrain and in the
CC pontine nucleus, cerebellar granule cells, and Purkinje cells in
CC the hindbrain.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
CC family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch)
CC
CC EMBL; U16845; AAA67445.1; -.
CC PIR; I56551; I56551.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC Pfam; PF00047; Ig_3.
CC SMART; SM00408; Igc2; 2.
CC PROSITE; PS50835; IG_LIKE; 3.
CC Cell adhesion; Direct protein sequencing; Glycoprotein; GPI-anchor;
CC Immunoglobulin domain; Lipoprotein; Repeat; Signal.
CC SIGNAL 1 33 Potential.
CC CHAIN 34 321 Neurotrophin.
CC PROPEP 322 344 Removed in mature form (Potential).
CC DOMAIN 39 126 Ig-like C2-type 1.
CC DOMAIN 136 218 Ig-like C2-type 2.
CC DOMAIN 222 309 Ig-like C2-type 3.
CC DISULFID 57 115 Potential.
CC DISULFID 157 201 Potential.
CC DISULFID 243 295 Potential.
CC CARBOHYD 44 44 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 70 70 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 152 152 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 216 216 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 284 284 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 305 305 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 321 321 N-linked (GlcNAc...) (Potential).
CC LIPID 321 321 GPI-anchor amidated asparagine
CC (Potential).
SQ SEQUENCE 344 AA; 37998 MW; CBB39BE53833B224 CRC64;

Query Match 90.8%; Score 1639.5; DB 1; Length 344;
Best Local Similarity 92.9%; Pred. No. 2.3e-122;
Matches 312; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

QY 12 ISWALFTGLAALCLF---QGVPRSGDATFPKAMDNVTVRQGESATLRCCTIDNRVTRVAV 68
Db 9 LPWKCLVWVSLRLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCCTIDNRVTRVAV 68

QY 69 LNRSTLYAGNDKWCLDRPVLLSNTQYISIEIQNVVDYDGGPYTCSVQTDNHPKTSRV 128
Db 69 LNRSTLYAGNDKWCLDRPVLLSNTQYISIEIQNVVDYDGGPYTCSVQTDNHPKTSRV 128

QY 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFVSEDEYLEI 188
Db 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFVSEDEYLEI 188

QY 189 QGITREQSDYECSSASNDVAAPVVRVKVTNNYPPISEAKGTGVPVQKGLQCEASAV 248
Db 189 QGITREQSDYECSSASNDVAAPVVRVKVTNNYPPISEAKGTGVPVQKGLQCEASAV 248

QY 249 PSAEFQWKDKRLLEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVSNKLGHTNASI 308
Db 249 PSAEFQWKDKRLLEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVSNKLGHTNASI 308

QY 309 MLFGGAVSEVNGTSRRAGCVLLPLLVHLLKLF 344
Db 309 MLFGGAVSEVNGTSRRAGCVLLPLLVHLLKLF 344
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CC -----
DR EMBL; AF126426; AAF37591.1; -
DR EMBL; AY358331; AAO88697.1; -
DR EMBL; BC050716; AAH50716.1; -
DR HSP; P13590; IIE5.
DR MIM; 607938; -
DR GO; GO:0008038; P:neural cell recognition; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; Igc2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Alternative splicing; Cell adhesion; Direct protein sequencing;
KW Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein; Repeat;
KW Signal.
FT SIGNAL 1 33
FT CHAIN 34 321
FT PROPEP 322 344
FT DOMAIN 39 126
FT DOMAIN 136 218
FT DOMAIN 222 309
FT DISULFID 57 115
FT DISULFID 157 201
FT DISULFID 243 295
FT CARBOHYD 44 44
FT CARBOHYD 70 70
FT CARBOHYD 152 152
FT CARBOHYD 284 284
FT CARBOHYD 292 292
FT CARBOHYD 305 305
FT CARBOHYD 321 321
FT LIPID 321 321
FT VARSPLIC 1 27
FT FTID=VSP 010939.
FT FTID=VSP 010941.
FT VARSPLIC 313 316
FT VARSPLIC 317 344
FT SEQUENCE 344 AA; 37971 MW; 34412C295ABBE3A CRC64;
Query Match 92.2%; Score 1665.5; DB 1; Length 344;
Best Local Similarity 95.2%; Pred. No. 1.9e-124;
Matches 320; Conservative 3; Mismatches 10; Indels 3; Gaps 1;
Qy 12 ISWAFTGLAALCLF---QGVFVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAV 68
Db 9 LPWKCLVVSURLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAV 68
Qy 69 LNRSTILYAGDKKCLDPRVLLNTQTSIEIQNVVDVDEGYTCSVQTDNHPKTSRV 128
Db 69 LNRSTILYAGDKKCLDPRVLLNTQTSIEIQNVVDVDEGYTCSVQTDNHPKTSRV 128
Qy 129 HLIIVQSPKIVEISSDISINEGNNISLTCIATGPEPTVWRHSIPKAVGVSEDEYLEI 188
Db 129 HLIIVQSPKIVEISSDISINEGNNISLTCIATGPEPTVWRHSIPKAVGVSEDEYLEI 188
Qy 189 QGITRESGDGYECASNDVAAPVVRVVKVTYVNPPIYSEAKGTGVPVQKGTLCQCEASAV 248
Db 189 QGITRESGDGYECASNDVAAPVVRVVKVTYVNPPIYSEAKGTGVPVQKGTLCQCEASAV 248
Qy 249 PSAEFQWKDKRLIEGKKGKVKVENRPFSLKLIFFNVSEHDYGYNTCVASNKLGHNTASI 308
Db 249 PSAEFQWKDKRLIEGKKGKVKVENRPFSLKLIFFNVSEHDYGYNTCVASNKLGHNTASI 308
Qy 309 MLFGPGAVSEVSGTSSRAGCVMLLLVLLHLKLF 344
Db 309 MLFGPGAVSEVSGTSSRAGCVMLLLVLLHLKLF 344
RESULT 3
NTRI_MOUSE

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ID NTRI_MOUSE STANDARD; PRT; 344 AA.
AC Q99PJ0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neurotrimin precursor.
GN Name=Nt; Synonyms=Hnt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT Sequencing pipeline with 384 multipillarary sequencer";
RL Genome Res. 10:1757-1771(2000).

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RP SEQUENCE FROM N.A. (ISOFORM 1)
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
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RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akai H., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK045973; BAC32555.1; -;
DR EMBL; AK046377; BAC32695.1; -;
DR HSSP; P13596; 1Q21.
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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
SQ SEQUENCE 344 AA; 37941 MW; CDA5295D4CD86065 CRC64;

Query Match 98.6%; Score 1780; DB 2; Length 344;
Best Local Similarity 98.0%; Pred. No. 1.5e-133;
Matches 337; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKTIQKMHNSISWIFGLAALCLFQGVPRSGDATPPKAMDNTVVRQGESATLRCTID 60
Db 1 MKTIQKMHNSISWIFGLAALCLFQGVPRSGDATPPKAMDNTVVRQGESATLRCTID 60

QY 61 NRVTRVAMLRNSTILYAGNDKWKCLDPVRLVLSNTQTSIEIQNVVDVYDEGPTCSVQTD 120
Db 61 NRVTRVAMLRNSTILYAGNDKWKCLDPVRLVLSNTQTSIEIQNVVDVYDEGPTCSVQTD 120

QY 121 NHPKTSRVHLIVQVSPKIVEISSDISEGNNISLTCTATGPEPTVTRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISEGNNISLTCTATGPEPTVTRHISPKAVGFV 180

QY 181 SEDEYLEIQITREGSDGYECASNDVAAPVRRVKVTWVPPYISEAKGTGVPVQKGT 240
Db 181 SEDEYLEIQITREGSDGYECASNDVAAPVRRVKVTWVPPYISEAKGTGVPVQKGT 240

QY 241 LOCEASAVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVSNK 300
Db 241 LOCEASAVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVSNK 300

QY 301 LGHTNASIMLFGPGAVSEVNGTSRRAGCVWLLPLLVLLHLK 344
Db 301 LGHTNASIMLFGPGAVSEVNGTSRRAGCVWLLPLLVLLHLK 344

RESULT 2

ID NTRI_HUMAN STANDARD; PRT; 344 AA.
AC Q9P121; Q6UXJ3; Q86VJ9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Neurotrophin precursor (NTP) (UNQ297/PRO337).
OS Name=NTP;
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).

RA Li G., Jin J., Tan X., Hu S., Yuan J., Qiang B.;
RT "Cloning and identification of human neurotrophin full length cDNA";
RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2)
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3)
RC TISSUE=Skin;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Stachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 34-48.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
CC -!- FUNCTION: Neural cell adhesion molecule.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q9P121-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9P121-2; Sequence=VSP_010939;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=Q9P121-3; Sequence=VSP_010940, VSP_010941;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
CC family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).

1419 123.5 6.8 574 1 IRL2_MOUSE
1420 123.5 6.8 640 1 DIM1_CAEEL
1421 123.5 6.8 645 2 Q6DR98
1422 123.5 6.8 978 1 KIT_FELCA
1423 123.5 6.8 1349 1 GLI6_RAT
1424 123 6.8 168 2 Q7Q6K5
1425 123 6.8 287 2 Q6QW80
1426 123 6.8 321 2 Q6UX14
1427 123 6.8 351 2 Q15225
1428 123 6.8 367 2 Q8T603
1429 123 6.8 399 2 Q9T279
1430 123 6.8 476 2 Q80WU0
1431 123 6.8 696 1 IPL1_HUMAN
1432 123 6.8 696 1 IPL1_PANTR
1433 123 6.8 707 2 P978E0
1434 123 6.8 821 1 TRKB_MOUSE
1435 123 6.8 1072 2 Q8T104
1436 123 6.8 1176 1 KMLS_BOVIN
1437 122.5 6.8 167 2 Q8NFN2
1438 122.5 6.8 211 2 Q7RTW5
1439 122.5 6.8 241 2 Q7RTW0
1440 122.5 6.8 316 1 FGA_PANTR
1441 122.5 6.8 326 1 V816_CWXPB
1442 122.5 6.8 326 2 Q77DR6
1443 122.5 6.8 394 2 Q6TGK9
1444 122.5 6.8 412 2 Q9R1E1
1445 122.5 6.8 462 2 Q7RTW1
1446 122.5 6.8 637 2 Q7RTW3
1447 122.5 6.8 639 1 NRG1_HUMAN
1448 122.5 6.8 640 2 Q7RTV8
1449 122.5 6.8 645 2 Q7RTW4
1450 122.5 6.8 662 1 NRG1_RAT
1451 122.5 6.8 785 2 Q7TNE4
1452 122.5 6.8 994 1 MERK_RAT
1453 122 6.8 272 2 Q8R1N5
1454 122 6.8 390 2 Q7QBR2
1455 122 6.8 397 2 Q09263
1456 122 6.8 458 1 CD4_MACFA
1457 122 6.8 459 2 Q8ZMD0
1458 122 6.8 606 2 Q9BZ20
1459 122 6.8 696 1 IPL1_PONPY
1460 122 6.8 696 1 IPL1_RAT
1461 122 6.8 850 1 NRG2_HUMAN
1462 122 6.8 923 2 Q97745
1463 122 6.8 953 2 Q8P619
1464 122 6.8 964 2 Q97744
1465 122 6.8 964 2 Q9TQ01
1466 122 6.8 1685 2 Q6H969
1467 122 6.8 1685 2 Q6ZU00
1468 121.5 6.7 155 2 Q8J1J7
1469 121.5 6.7 305 2 Q8PJF0
1470 121.5 6.7 332 1 PSGB_HUMAN
1471 121.5 6.7 365 2 Q9BWMV3
1472 121.5 6.7 390 2 Q96AP7
1473 121.5 6.7 390 2 Q96T50
1474 121.5 6.7 412 2 Q63111
1475 121.5 6.7 558 2 Q8PDB1
1476 121.5 6.7 637 2 Q8NSG0
1477 121.5 6.7 818 1 TRKB_CHICK
1478 121.5 6.7 821 1 TRKB_RAT
1479 121.5 6.7 1450 1 MP5F_CHICK
1480 121 6.7 223 2 Q8N6G0
1481 121 6.7 277 2 Q8IRE8
1482 121 6.7 281 2 P97546
1483 121 6.7 292 2 Q9N168
1484 121 6.7 292 2 Q57146
1485 121 6.7 292 2 Q78517
1486 121 6.7 303 2 Q7ZXR4
1487 121 6.7 305 2 Q8P3R4
1488 121 6.7 532 2 Q9SR30
1489 121 6.7 733 2 Q60830
1490 121 6.7 733 2 Q80T10
1491 121 6.7 994 1 MERK_MOUSE

Q9ers7 mus musculus
Q18066 caenorhabdi
Q6dr98 mus musculus
Q28889 felis silve
Q9wvt0 rattus norv
Q7gk5 anopheles g
Q9w80 mus sp. . f
Q6ux14 homo sapien
Q15225 homo sapien
Q8t603 drosophila
Q9y279 homo sapien
Q80w00 mus musculus
Q9nzn1 homo sapien
P60029 pan troglod
P97860 mus musculus
P15209 mus musculus
Q8t104 bombyx mori
Q28824 bos taurus
Q8nfn2 homo sapien
Q7rtw5 homo sapien
Q7rtw0 homo sapien
Q8spv8 pan troglod
Q4523 cowpox viru
Q77dr6 cowpox viru
Q6tgk9 oryctolagus
Q9r1e1 rattus norv
Q7rtw1 homo sapien
Q7rtw3 homo sapien
Q02297 h pro-neure
Q7rtv8 homo sapien
Q7rtw4 homo sapien
P43322 r pro-neure
Q7tnd4 mus musculus
P57097 rattus norv
Q8rln5 mus musculus
Q7qbr2 anopheles g
Q09263 cercopithec
P97185 macaca fasc
Q8zmd0 homo sapien
Q9bz20 homo sapien
Q7yql9 pongo pygma
P59824 rattus norv
Q14511 homo sapien
Q97745
Q8p6y3 xenopus lae
Q97744 sus scrofa
Q8tqql sus scrofa
Q6h969 homo sapien
Q6zuu0 homo sapien
Q8j1j7 mus musculus
Q8pjp0 homo sapien
Q8uq72 homo sapien
Q8wmv3 bos taurus
Q96ap7 homo sapien
Q96t50 homo sapien
Q63111 rattus norv
Q8pdl1 homo sapien
Q8ns90 homo sapien
Q91987 gallus gall
Q63604 rattus norv
Q02173 gallus gall
Q8nbc0 drosophila
Q8ire8 rattus norv
P97546 rattus norv
Q9n168 papio hanad
Q57146 human herpe
Q78517 human herpe
Q7zxr4 xenopus lae
Q8p3a4 mus musculus
Q9sr30 drosophila
Q60830 mus musculus
Q80t10 mus musculus
Q60805 mus musculus

1492 121 6.7 1035 2 Q9NEG1
1493 121 6.7 1142 1 MYPF_HUMAN
1494 121 6.7 1333 2 Q7PT57
1495 120.5 6.7 284 2 Q9NX42
1496 120.5 6.7 316 2 Q8VE98
1497 120.5 6.7 316 2 Q7TPB4
1498 120.5 6.7 353 2 Q63242
1499 120.5 6.7 461 2 Q35947
1500 120.5 6.7 468 2 Q6PJ50

Q9neg1 drosophila
Q14324 homo sapien
Q7pt57 anopheles g
Q9nx42 homo sapien
Q8ve98 mus musculus
Q7tpb4 rattus norv
Q63242 rattus norv
Q35947 mesocricetu
Q6pj50 mus musculus

ALIGNMENTS

RESULT 1

Q8BG33 PRELIMINARY; PRT; 344 AA.

ID Q8BG33;
AC Q8BG33;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
DE enriched library, clone:B230328N06 product:NEUROTRIMIN (GP65) homolog
DE (Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
DE enriched library, clone:B230377K17 product:NEUROTRIMIN (GP65)
DE homolog)
GN Name=Rnt;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

1273	130.5	7.2	775	2	097754	097754	oryctolagus	1346	126.5	7.0	722	2	Q6GNB3	Q6gnb3	xenopus lae
1274	130.5	7.2	873	2	Q98949	Q98949	gallus gall	1347	126.5	7.0	723	2	Q86YI4	Q86y14	homo sapien
1275	130	7.2	325	2	Q95791	Q95791	homo sapien	1348	126.5	7.0	945	2	O77589	O77589	equus caball
1276	130	7.2	332	1	CD22_PANPA	Q9n1e5	pan paniscu	1349	126.5	7.0	1099	2	O7TMR8	O7tmr8	mus musculus
1277	130	7.2	332	1	CD22_PANTR	Q9n1e6	pan paniscu	1350	126.5	7.0	1212	2	O95TGO	O95tgo	drosohila
1278	130	7.2	394	2	Q925F2	Q925f2	mus musculus	1351	126	7.0	168	2	Q8MI25	Q8mi25	ovis aries
1279	130	7.2	697	2	Q922E0	Q922e0	mus musculus	1352	126	7.0	204	2	Q63ZH7	Q63zh7	xenopus lae
1280	130	7.2	727	1	PEC1_MOUSE	Q08481	mus musculus	1353	126	7.0	553	2	Q8WXJ5	Q8wxj5	homo sapien
1281	130	7.2	732	2	Q8CAW4	Q8caw4	mus musculus	1354	126	7.0	822	1	TRKB_HUMAN	Q9dtk3	homo sapien
1282	129.5	7.2	208	2	Q866T1	Q866t1	pongo pygma	1355	126	7.0	828	2	Q9DGK3	Q9dtk3	xenopus lae
1283	129.5	7.2	272	2	Q701Q2	Q7qlq2	anopheles g	1356	126	7.0	838	2	Q8WXJ7	Q8wxj7	homo sapien
1284	129.5	7.2	346	2	Q92027	P92027	drosohila	1357	125.5	6.9	251	2	Q99970	Q99970	caenorhabdi
1285	129.5	7.2	365	2	Q6VAN5	Q6van5	bos taurus	1358	125.5	6.9	278	2	Q61350	Q61350	mus musculus
1286	129.5	7.2	372	2	Q6VAN6	Q6van6	bos taurus	1359	125.5	6.9	341	2	Q61353	Q61353	mus musculus
1287	129.5	7.2	415	2	Q60977	Q60977	mus musculus	1360	125.5	6.9	342	2	P97635	P97635	rattus norv
1288	129.5	7.2	436	2	Q6VAN8	Q6van8	bos taurus	1361	125.5	6.9	524	2	Q810V7	Q810v7	dugesia jap
1289	129.5	7.2	582	2	Q80WN2	Q80wn2	mus musculus	1362	125.5	6.9	525	2	Q9W0L9	Q9w0l9	drosohila
1290	129.5	7.2	595	2	Q68SN8	Q68sn8	mus musculus	1363	125.5	6.9	526	1	BUTY_HUMAN	Q13410	homo sapien
1291	129.5	7.2	771	2	Q8N1I6	Q8n1i6	homo sapien	1364	125.5	6.9	787	2	Q8K061	Q8k061	mus musculus
1292	129.5	7.2	967	2	Q76KE8	Q76ke8	oncorhynch	1365	125.5	6.9	829	2	Q9PSV8	Q9psv8	xenopus lae
1293	129.5	7.2	975	1	KIT_CANFA	Q97799	canis famil	1366	125.5	6.9	975	1	KIT_MOUSE	P05532	mus musculus
1294	129.5	7.2	975	2	Q7YRV7	Q7yrv7	canis famil	1367	125.5	6.9	975	2	Q6QJB7	Q6qjb7	mus musculus
1295	129.5	7.2	979	2	Q8WN23	Q8wn23	canis famil	1368	125.5	6.9	975	2	Q6QJB8	Q6qjb8	mus musculus
1296	129.5	7.2	987	2	Q7YZM8	Q7yzm8	caenorhabdi	1369	125.5	6.9	975	2	Q7TS86	Q7ts86	mus musculus
1297	129.5	7.2	1040	1	EG15_CABEL	Q10656	caenorhabdi	1370	125.5	6.9	979	2	Q8C8K9	Q8c8k9	mus musculus
1298	129.5	7.2	1051	2	Q7JL68	Q7jl68	caenorhabdi	1371	125.5	6.9	1031	2	Q80YN7	Q80yn7	mus musculus
1299	129.5	7.2	1096	2	Q8MQ14	Q8mq14	caenorhabdi	1372	125.5	6.9	10578	2	Q81SF5	Q81sf5	caenorhabdi
1300	129	7.1	306	2	Q90YL4	Q90yl4	mus musculus	1373	125	6.9	370	2	Q7TSN7	Q7tsn7	mus musculus
1301	129	7.1	321	2	Q9DEE3	Q9dee3	gallus gall	1374	125	6.9	398	2	Q9Y640	Q9y640	homo sapien
1302	129	7.1	328	2	Q6ZWC9	Q6zwc9	homo sapien	1375	125	6.9	707	2	Q8CBC6	Q8cbc6	mus musculus
1303	129	7.1	417	1	PVR_HUMAN	P15151	homo sapien	1376	125	6.9	876	2	Q7PW78	Q7pw78	anopheles g
1304	129	7.1	486	2	Q9DEE2	Q9dee2	gallus gall	1377	125	6.9	964	2	Q9TQO0	Q9tqo0	sus scrofa
1305	129	7.1	533	2	Q9DEE1	Q9dee1	gallus gall	1378	125	6.9	977	1	KIT_BOVIN	P43481	bos taurus
1306	129	7.1	1098	1	PGDR_MOUSE	P05622	mus musculus	1379	125	6.9	978	1	KIT_CAPI	Q28317	capra hircu
1307	128.5	7.1	213	2	Q9N167	Q9n167	papio hamad	1380	125	6.9	1062	2	Q8AXC7	Q8axc7	fugu rubrip
1308	128.5	7.1	226	2	Q7PYG1	Q7pyg1	anopheles g	1381	125	6.9	1078	2	Q8AXC8	Q8axc8	fugu rubrip
1309	128.5	7.1	268	2	Q46603	Q46603	sus scrofa	1382	124.5	6.9	145	2	Q9MZE4	Q9mze4	macaca mula
1310	128.5	7.1	477	2	Q6UXJ4	Q6uxj4	homo sapien	1383	124.5	6.9	192	2	Q9SERP7	Q9serp7	rattus norv
1311	128.5	7.1	515	1	PVR1_MOUSE	Q9j1kf6	mus musculus	1384	124.5	6.9	244	2	Q9ST89	Q9st89	drosohila
1312	128.5	7.1	515	2	Q6P9M9	Q6p9m9	mus musculus	1385	124.5	6.9	311	2	Q6DN73	Q6dn73	homo sapien
1313	128.5	7.1	595	1	SILL_HUMAN	Q95pq1	homo sapien	1386	124.5	6.9	496	2	Q6ZTG1	Q6ztg1	homo sapien
1314	128.5	7.1	733	2	Q9QZM7	Q9qzm7	mus musculus	1387	124.5	6.9	499	2	Q7Z728	Q7z728	homo sapien
1315	128	7.1	240	2	Q6TYZ5	Q6tyz5	canis famil	1388	124.5	6.9	504	2	Q98923	Q98923	gallus gall
1316	128	7.1	319	2	Q9YTU0	Q9ytu0	canis famil	1389	124.5	6.9	731	2	Q91150	Q91150	notophthalm
1317	128	7.1	769	2	Q8N1I5	Q8n1i5	homo sapien	1390	124.5	6.9	828	2	Q91743	Q91743	xenopus lae
1318	128	7.1	806	1	FGR3_HUMAN	P22607	homo sapien	1391	124.5	6.9	960	1	KIT_CHICK	Q08156	gallus gall
1319	128	7.1	1129	2	Q80UX0	Q80ux0	mus musculus	1392	124	6.9	259	2	Q7Z2Q1	Q7z2q1	homo sapien
1320	128	7.1	1214	2	Q75054	Q75054	homo sapien	1393	124	6.9	278	2	Q99232	Q99232	mus musculus
1321	128	7.1	1427	2	Q9VZT8	Q9vzt8	drosohila	1394	124	6.9	341	2	Q61354	Q61354	mus musculus
1322	127.5	7.1	94	2	Q9VRI14	Q9vri14	drosohila	1395	124	6.9	426	1	PSG9_HUMAN	Q00887	homo sapien
1323	127.5	7.1	241	2	Q07112	Q07112	bos taurus	1396	124	6.9	650	2	Q63709	Q63709	rattus sp.
1324	127.5	7.1	271	1	OX2V_HHV8	P88963	human herpe	1397	124	6.9	812	2	Q69ZJ6	Q69zj6	mus musculus
1325	127.5	7.1	271	2	Q40948	Q40948	human herpe	1398	124	6.9	972	2	Q26614	Q26614	strongyloce
1326	127.5	7.1	329	2	Q92178	Q92178	mus musculus	1399	124	6.9	993	1	FLT3_HUMAN	P38888	homo sapien
1327	127.5	7.1	388	1	BASI_RAT	P26453	rattus norv	1400	124	6.9	999	1	MERK_HUMAN	Q12866	homo sapien
1328	127.5	7.1	390	2	Q9SK13	Q9sk13	macaca fasc	1401	124	6.9	1124	2	Q6P6L5	Q6p6l5	mus musculus
1329	127.5	7.1	499	1	SIL8_HUMAN	Q9nyz4	homo sapien	1402	124	6.9	1294	2	Q80TB0	Q80tb0	mus musculus
1330	127.5	7.1	926	2	Q7LDM3	Q7ldm3	homo sapien	1403	124	6.9	1569	2	Q6PAC0	Q6pac0	mus musculus
1331	127	7.0	330	1	CD22_PONPY	Q9n1e3	pongo pygma	1404	124	6.9	1666	1	MYM1_MOUSE	Q62234	mus musculus
1332	127	7.0	406	2	Q8BR20	Q8br20	mus musculus	1405	123.5	6.8	181	2	Q91665	Q91665	xenopus lae
1333	127	7.0	452	2	Q70355	Q70355	mus musculus	1406	123.5	6.8	211	2	Q8BK18	Q8bk18	mus musculus
1334	127	7.0	595	2	Q90720	Q90720	gallus gall	1407	123.5	6.8	231	2	Q8WYV6	Q8wyv6	homo sapien
1335	127	7.0	658	2	Q8NHN4	Q8nhn4	homo sapien	1408	123.5	6.8	241	2	Q6PK61	Q6pk61	homo sapien
1336	127	7.0	879	1	FRP_MOUSE	Q9wv91	mus musculus	1409	123.5	6.8	253	2	Q9D8H2	Q9d8h2	m mus muscu
1337	127	7.0	992	1	FLT3_MOUSE	Q00342	mus musculus	1410	123.5	6.8	257	2	Q8R202	Q8r202	mus musculus
1338	126.5	7.0	295	2	Q9ERF5	Q9erf5	mesocricetu	1411	123.5	6.8	261	2	Q9D7L8	Q9d7l8	m mus muscu
1339	126.5	7.0	305	2	Q6ZS95	Q6zs95	homo sapien	1412	123.5	6.8	285	2	Q9D780	Q9d780	mus musculus
1340	126.5	7.0	340	2	Q61349	Q61349	mus musculus	1413	123.5	6.8	285	2	Q8VE93	Q8ve93	mus musculus
1341	126.5	7.0	344	1	Q9UKV4	Q9ukv4	homo sapien	1414	123.5	6.8	357	2	Q8SPW5	Q8spw5	macaca fasc
1342	126.5	7.0	365	1	CXAR_HUMAN	P78310	homo sapien	1415	123.5	6.8	402	2	Q15227	Q15227	homo sapien
1343	126.5	7.0	466	2	Q9S5I0	Q9se10	drosohila	1416	123.5	6.8	403	2	Q8HY15	Q8hy15	lemur catia
1344	126.5	7.0	516	2	Q6PHF8	Q6phf8	brachydanio	1417	123.5	6.8	501	2	Q6GMJ2	Q6gmj2	brachydanio
1345	126.5	7.0	677	1	NRG1_XENLA	Q93383	xenopus lae	1418	123.5	6.8	516	2	Q6NWX4	Q6nw94	brachydanio

1127	137	7.6	424	1	PSGA_HUMAN	Q15235	homo sapien	1200	133.5	7.4	888	1	UFO_MOUSE	Q00993	mus musculus
1128	137	7.6	448	2	Q8IGF5	Q8iga5	drosophila	1201	133.5	7.4	888	2	Q80YQ3	Q80yq3	mus musculus
1129	137	7.6	448	2	Q8JHL7	Q8jhl7	rattus norv	1202	133.5	7.4	888	2	Q6PUB9	Q6pub9	ambystoma m
1130	137	7.6	458	2	Q830P3	Q830p3	rattus norv	1203	133.5	7.4	1598	2	Q9P214	Q9p214	homo sapien
1131	137	7.6	459	2	Q9JHL6	Q9jhl6	rattus norv	1204	133	7.4	317	2	Q9ESA2	Q9esa2	rattus norv
1132	137	7.6	517	1	PVR1_HUMAN	Q15223	homo sapien	1205	133	7.4	323	2	Q9ESA3	Q9esa3	rattus norv
1133	137	7.6	662	2	Q8MQZ9	Q8mqz9	drosophila	1206	133	7.4	366	2	Q9N680	Q9n680	drosophila
1134	137	7.6	662	2	Q9VGQD	Q9vgqd	drosophila	1207	133	7.4	383	2	Q18431	Q18431	geodia cydo
1135	137	7.6	778	1	TRKA_CHICK	Q81009	gallus gall	1208	133	7.4	541	2	Q95XJ7	Q95xj7	caenorhabdi
1136	137	7.6	977	2	Q88ST2	Q88su2	danio kerr	1209	133	7.4	612	2	Q96CY4	Q96cy4	homo sapien
1137	136.5	7.6	345	2	Q7PVU1	Q7pvu1	anopheles g	1210	133	7.4	802	1	FGR4_HUMAN	P22455	homo sapien
1138	136.5	7.6	459	2	Q86X91	Q86x91	homo sapien	1211	133	7.4	802	2	Q8TDA0	P22455	homo sapien
1139	136.5	7.6	498	2	Q9UBF9	Q9ubf9	homo sapien	1212	133	7.4	807	2	Q6DD66	Q6dd66	anopheles lae
1140	136.5	7.6	677	2	Q8QHL2	Q8qhl2	gallus gall	1213	133	7.4	818	2	Q91742	Q91742	anopheles lae
1141	136.5	7.6	738	1	PECL1_HUMAN	Q81284	homo sapien	1214	133	7.4	818	2	Q9PSV9	Q9psv9	anopheles lae
1142	136.5	7.6	3100	2	Q7KTY5	Q7kyn5	homo sapien	1215	133	7.4	839	1	TRKC_HUMAN	Q62888	homo sapien
1143	136	7.5	229	2	Q7Q9S4	Q7q9s4	anopheles g	1216	133	7.4	839	2	Q7S682	Q7s682	homo sapien
1144	136	7.5	298	2	Q8C5K9	Q8c5k9	mus musculus	1217	133	7.4	974	2	Q98SU3	Q98su3	danio dangi
1145	136	7.5	298	2	Q8CEJ95	Q8cej95	mus musculus	1218	133	7.4	1091	2	Q9YH41	Q9yh41	gallus gall
1146	136	7.5	298	2	Q8J159	Q8j159	m vascular	1219	132.5	7.3	393	2	P97547	P97547	rattus norv
1147	136	7.5	393	2	Q85727	Q85727	homo sapien	1220	132.5	7.3	411	2	Q15228	Q15228	homo sapien
1148	136	7.5	906	2	Q8N9C0	Q8n9c0	homo sapien	1221	132.5	7.3	419	2	Q68CR6	Q68cr6	homo sapien
1149	136	7.5	976	2	Q8NFR5	Q8jfr5	brachydanio	1222	132.5	7.3	419	2	Q6P520	Q6p520	homo sapien
1150	135.5	7.5	232	2	Q7PJL8	Q7pj18	anopheles g	1223	132.5	7.3	423	2	Q8BU57	Q8bu57	mus musculus
1151	135.5	7.5	326	2	Q9N166	Q9n166	papio hamad	1224	132.5	7.3	426	1	PSG8_HUMAN	Q9uq74	homo sapien
1152	135.5	7.5	442	2	Q7PT04	Q7pt04	anopheles g	1225	132.5	7.3	492	2	Q7QD44	Q7qd44	anopheles g
1153	135.5	7.5	762	2	Q91TW8	Q91tw8	homo sapien	1226	132.5	7.3	533	2	Q8NCB6	Q8ncb6	homo sapien
1154	135.5	7.5	822	2	Q91288	Q91288	pleurodeles	1227	132.5	7.3	534	2	Q8NBI8	Q8nb18	homo sapien
1155	135.5	7.5	975	2	P79750	P79750	fugu rubrip	1228	132.5	7.3	584	2	Q90989	Q90989	gallus gall
1156	135.5	7.5	13133	2	Q71A42	Q71a42	caenorhabdi	1229	132.5	7.3	620	2	Q61GL3	Q61gl3	drosophila
1157	135	7.5	332	2	Q640U3	Q640u3	anopheles tro	1230	132.5	7.3	626	2	Q90880	Q90880	gallus gall
1158	135	7.5	393	2	Q6IRX2	Q6irx2	homo sapien	1231	132.5	7.3	671	2	Q63711	Q63711	rattus ratt
1159	135	7.5	464	2	Q8GLZ5	Q8glz5	anopheles tro	1232	132.5	7.3	800	2	Q9JHX9	Q9jhx9	rattus norv
1160	135	7.5	802	2	Q95M13	Q95m13	bos taurus	1233	132.5	7.3	856	2	Q62121	Q62121	mus musculus
1161	135	7.5	817	2	Q8JG38	Q8jg38	brachydanio	1234	132.5	7.3	1087	2	Q9PUF6	Q9pu66	gallus gall
1162	134.5	7.4	242	2	Q46604	Q46604	sus scrofa	1235	132	7.3	201	2	Q7PX42	Q7px42	anopheles g
1163	134.5	7.4	263	2	Q7TPW5	Q7tpw5	mus musculus	1236	132	7.3	387	2	Q86XK7	Q86xk7	homo sapien
1164	134.5	7.4	348	2	Q8NFN3	Q8nfn3	homo sapien	1237	132	7.3	408	2	Q8K094	Q8k094	m hypotheti
1165	134.5	7.4	419	1	PSG7_HUMAN	Q13046	homo sapien	1238	132	7.3	412	2	Q6MZ84	Q6mz84	homo sapien
1166	134.5	7.4	426	2	Q64HX5	Q64hx5	oncorhynch	1239	132	7.3	502	2	Q92ZQ0	Q92zq0	mus musculus
1167	134.5	7.4	428	1	PSG3_HUMAN	Q16557	homo sapien	1240	132	7.3	582	2	Q95N25	Q95n25	bos taurus
1168	134.5	7.4	480	2	Q9PSD1	Q9psd1	anopheles fi	1241	132	7.3	992	2	Q8AXU0	Q8axu0	oncorhynch
1169	134.5	7.4	493	2	Q6P5Y4	Q6p5y4	homo sapien	1242	132	7.3	1048	2	P79749	P79749	fugu rubrip
1170	134.5	7.4	531	2	Q659F2	Q659f2	homo sapien	1243	131.5	7.3	298	1	JAM2_HUMAN	P57087	homo sapien
1171	134.5	7.4	659	2	Q6ZNM1	Q6znm1	homo sapien	1244	131.5	7.3	298	2	Q6YNC1	Q6ync1	homo sapien
1172	134.5	7.4	660	2	Q7Z6B1	Q7z6b1	homo sapien	1245	131.5	7.3	312	2	Q6UXG6	Q6uxg6	homo sapien
1173	134.5	7.4	782	2	Q80TU8	Q80tu8	mus musculus	1246	131.5	7.3	370	2	Q6MZQ3	Q6mzq3	homo sapien
1174	134.5	7.4	1205	2	Q8BUJ0	Q8bu10	mus musculus	1247	131.5	7.3	480	2	Q9PSC9	Q9psc9	anopheles fi
1175	134.5	7.4	1235	2	Q95428	Q95428	homo sapien	1248	131.5	7.3	739	2	Q865F2	Q865f2	oryctolagus
1176	134.5	7.4	19066	2	Q801W8	Q801w8	brachydanio	1249	131.5	7.3	814	2	Q6GNP8	Q6gnp8	anopheles lae
1177	134	7.4	217	2	Q8KGN0	Q8kgn0	bacterioph	1250	131	7.3	259	2	Q8WR47	Q8wr47	caenorhabdi
1178	134	7.4	238	2	Q20339	Q20339	caenorhabdi	1251	131	7.3	298	2	Q9GL74	Q9gl74	carcophithe
1179	134	7.4	283	2	Q9VNK0	Q9vnk0	drosophila	1252	131	7.3	327	2	Q961Q7	Q961q7	homo sapien
1180	134	7.4	294	2	Q6KGN1	Q6kgn1	bacterioph	1253	131	7.3	330	2	Q63241	Q63241	rattus norv
1181	134	7.4	321	2	Q9DEB6	Q9deb6	gallus gall	1254	131	7.3	342	2	Q9ESAI	Q9esai	rattus norv
1182	134	7.4	397	2	Q8XRC3	Q8xrc3	homo sapien	1255	131	7.3	355	2	Q7Q1W7	Q7q1w7	anopheles g
1183	134	7.4	486	2	Q9DEB4	Q9dee4	gallus gall	1256	131	7.3	408	2	Q91WP1	Q91wp1	mus musculus
1184	134	7.4	533	2	Q9DEB5	Q9dee5	gallus gall	1257	131	7.3	408	2	Q8BVF6	Q8bvf6	mus musculus
1185	134	7.4	612	2	Q92Z29	Q92z29	mus musculus	1258	131	7.3	429	2	Q6VAN7	Q6van7	bos taurus
1186	134	7.4	825	2	Q6VNS1	Q6vns1	mus musculus	1259	131	7.3	782	2	Q9ESA5	Q9esa5	rattus norv
1187	134	7.4	864	1	TRKC_RAT	Q03351	rattus norv	1260	131	7.3	935	2	Q640T5	Q640t5	anopheles tro
1188	134	7.4	1147	1	KWLS_RABIT	P92994	oryctolagus	1261	131	7.3	978	2	Q9XS93	Q9xs93	canis famil
1189	133.5	7.4	283	2	Q7QGT4	Q7qgt4	anopheles g	1262	131	7.3	1097	1	FGDR_RAT	Q95030	rattus norv
1190	133.5	7.4	289	2	Q9QY15	Q9qy15	mus musculus	1263	131	7.3	1106	1	FGDR_HUMAN	P09619	homo sapien
1191	133.5	7.4	332	2	Q9P359	Q9p359	anopheles tro	1264	130.5	7.2	295	2	Q9QYL6	Q9qyl6	bos taurus
1192	133.5	7.4	335	1	PSG2_HUMAN	P11465	homo sapien	1265	130.5	7.2	295	2	Q9Z2H8	Q9z2h8	mus musculus
1193	133.5	7.4	374	2	Q7QB78	Q7qb78	anopheles g	1266	130.5	7.2	295	2	Q9Z2H8	Q9z2h8	mus musculus
1194	133.5	7.4	584	2	Q88921	Q88921	gallus gall	1267	130.5	7.2	310	1	FCGB_HUMAN	P31994	homo sapien
1195	133.5	7.4	597	1	SILL_PANTR	Q951h0	pan troglod	1268	130.5	7.2	323	1	FCGC_HUMAN	P31995	homo sapien
1196	133.5	7.4	626	2	Q98922	Q98922	gallus gall	1269	130.5	7.2	385	1	BASI_HUMAN	Q80ze2	mus musculus
1197	133.5	7.4	729	1	FGR1_DROME	Q07407	drosophila	1270	130.5	7.2	523	2	Q80ZE2	Q80ze2	mus musculus
1198	133.5	7.4	755	2	Q8CCF8	Q8ccf8	mus musculus	1271	130.5	7.2	569	1	SILF_MOUSE	Q920g3	mus musculus
1199	133.5	7.4	879	2	Q6PE80	Q6pe80	mus musculus	1272	130.5	7.2	707	2	Q9TT07	Q9tt07	canis famil

981	145.5	8.1	808	1	FGR4_MOUSE	Q03142	mus musculus	1054	141	7.8	821	1	FGR2_HUMAN	P21802	homo sapien
982	145.5	8.1	831	2	Q71SY9	Q71sy9	gallus gall	1055	141	7.8	879	2	Q8VI19	Q8vi19	rattus norv
983	145.5	8.1	1012	1	ROB4_MOUSE	Q8c310	mus musculus	1056	141	7.8	888	2	Q8VIA0	Q8via0	rattus norv
984	145.5	8.1	1898	2	Q64604	Q64604	r protein-t	1057	141	7.8	977	2	Q98SU1	Q98su1	danio nigro
985	145	8.0	259	2	Q9Y5B2	Q9y5b2	homo sapien	1058	140.5	7.8	705	2	Q83710	Q83710	rattus ratt
986	145	8.0	373	2	Q920S5	Q920s5	mus musculus	1059	140.5	7.8	737	2	Q965M3	Q965m3	caenorhabdi
987	145	8.0	622	2	Q9ES55	Q9ess5	mus musculus	1060	140.5	7.8	743	2	Q6P4H5	Q6p4h5	homo sapien
988	145	8.0	782	2	Q9TT23	Q9tt23	oryctolagus	1061	140.5	7.8	790	2	Q90699	Q90699	gallus gall
989	145	8.0	812	2	Q8MZ57	Q8mz57	drosophila	1062	140.5	7.8	823	1	CEK3_CHICK	P18461	gallus gall
990	145	8.0	878	2	Q9GV22	Q9gv22	mytilus gal	1063	140.5	7.8	1079	2	Q6E7F6	Q6e7f6	canis famil
991	145	8.0	972	1	KFMS_HUMAN	P07333	homo sapien	1064	140.5	7.8	1089	1	PGDS_HUMAN	P16234	homo sapien
992	145	8.0	972	2	Q86VW7	Q86vw7	homo sapien	1065	140.5	7.8	2164	2	Q91AR9	Q91ar9	gallus gall
993	145	8.0	1450	2	Q7QCP2	Q7qcp2	anopheles g	1066	140	7.8	562	2	Q6YNR7	Q6ynr7	brachydanio
994	144.5	8.0	203	2	Q7PVM1	Q7pvm1	anopheles g	1067	140	7.8	650	2	Q9R069	Q9r069	mus musculus
995	144.5	8.0	421	2	Q9NBB2	Q9nbb2	drosophila	1068	140	7.8	622	2	Q99K86	Q99k86	mus musculus
996	144.5	8.0	606	2	Q61RH8	Q61rh8	rattus norv	1069	140	7.8	738	2	Q7QJK6	Q7qjk6	anopheles g
997	144.5	8.0	739	2	Q8K0X1	Q8k0x1	mus musculus	1070	140	7.8	752	2	Q9XYS4	Q9xy84	hydra atten
998	144.5	8.0	754	2	Q8BZ76	Q8bz76	m mus muscu	1071	140	7.8	800	2	Q99052	Q99052	mus musculus
999	144.5	8.0	880	2	Q8QFP9	Q8qfp9	xenopus lae	1072	140	7.8	800	2	Q7TSI8	Q7tsi8	mus musculus
1000	144	8.0	260	2	Q7EP23	Q7ep23	anopheles g	1073	140	7.8	800	2	Q918X3	Q918x3	brachydanio
1001	144	8.0	278	2	Q6QYL3	Q6qyl3	mus musculus	1074	140	7.8	801	1	FGR3_MOUSE	Q91851	mus musculus
1002	144	8.0	413	2	Q6ZNI1	Q6zni1	homo sapien	1075	140	7.8	879	1	FRP_HUMAN	Q9p2b2	homo sapien
1003	144	8.0	422	2	Q8WR61	Q8wr61	lymantria d	1076	140	7.8	890	1	TYO3_HUMAN	Q06418	homo sapien
1004	144	8.0	434	2	Q6DN72	Q6dn72	homo sapien	1077	140	7.8	890	2	Q86VR3	Q86vr3	homo sapien
1005	144	8.0	438	2	Q9JLB7	Q9jlb7	mus musculus	1078	140	7.8	892	2	Q99662	Q99662	homo sapien
1006	144	8.0	510	2	Q9JLB8	Q9jlb8	mus musculus	1079	140	7.8	976	1	KIT_HUMAN	P10721	homo sapien
1007	144	8.0	542	2	Q8NHN5	Q8nhn5	homo sapien	1080	140	7.8	976	2	Q6IQ28	Q6iq28	homo sapien
1008	144	8.0	891	2	Q25177	Q25177	hydra atten	1081	140	7.8	1097	2	Q7QCP0	Q7qcp0	anopheles g
1009	143.5	7.9	296	2	Q640C0	Q640c0	xenopus lae	1082	140	7.8	2888	2	Q8MMK1	Q8mmk1	bombyx mori
1010	143.5	7.9	300	2	Q7SYQ7	Q7syq7	xenopus lae	1083	140	7.8	3239	2	Q8T102	Q8t102	bombyx mori
1011	143.5	7.9	430	2	Q8N4F1	Q8n4f1	homo sapien	1084	140	7.8	4203	2	Q9N5G2	Q9n5g2	caenorhabdi
1012	143.5	7.9	1177	2	Q21391	Q21391	caenorhabdi	1085	140	7.8	4219	2	Q9NL87	Q9nl87	caenorhabdi
1013	143.5	7.9	12268	2	Q8MQ08	Q8mq08	caenorhabdi	1086	140	7.8	4369	2	Q8MXD7	Q8mxd7	caenorhabdi
1014	143.5	7.9	13100	2	Q09165	Q09165	caenorhabdi	1087	140	7.8	4447	2	Q8MXD8	Q8mxd8	caenorhabdi
1015	143	7.9	442	2	Q8C306	Q8c306	mus musculus	1088	140	7.8	4488	2	Q9TXK2	Q9txk2	caenorhabdi
1016	143	7.9	620	1	SMP_CONJA	Q92154	coturnix co	1089	139.5	7.7	419	1	PSG1_HUMAN	P11464	homo sapien
1017	143	7.9	688	2	Q55095	Q55095	mus musculus	1090	139.5	7.7	422	2	Q96PJ3	Q96pj3	homo sapien
1018	143	7.9	688	2	Q8K1H4	Q8k1h4	mus musculus	1091	139.5	7.7	515	2	Q96PJ5	Q96pj5	homo sapien
1019	143	7.9	814	2	Q9VNP2	Q9vnp2	drosophila	1092	139.5	7.7	544	2	Q7ZY97	Q7zy97	xenopus lae
1020	143	7.9	972	2	Q761I0	Q761i0	callithrix	1093	139.5	7.7	670	2	Q7Z247	Q7zz47	brachydanio
1021	143	7.9	977	2	Q918N6	Q918n6	brachydanio	1094	139.5	7.7	739	2	Q28260	Q28260	canis famil
1022	143	7.9	1011	2	Q24273	Q24273	drosophila	1095	139.5	7.7	743	2	Q8P1M7	Q8p1m7	homo sapien
1023	143	7.9	1383	2	Q7Q840	Q7q840	anopheles g	1096	139.5	7.7	821	1	FGR2_MOUSE	P21803	mus musculus
1024	142.5	7.9	324	2	Q8NBY8	Q8nby8	homo sapien	1097	139.5	7.7	1052	1	FGR2_DROME	Q09147	drosophila
1025	142.5	7.9	326	2	Q9UPK8	Q9upk8	homo sapien	1098	139.5	7.7	1200	2	Q676A1	Q676a1	oikopleura
1026	142.5	7.9	435	1	PSG6_HUMAN	Q00889	homo sapien	1099	139	7.7	403	2	Q6NZV3	Q6nzv3	brachydanio
1027	142.5	7.9	515	2	Q96RE0	Q96re0	homo sapien	1100	139	7.7	416	2	Q96360	Q96360	hyphantria
1028	142.5	7.9	715	2	Q9NKA6	Q9nka6	drosophila	1101	139	7.7	763	2	Q95YM9	Q95ym9	pleurodeles
1029	142.5	7.9	739	1	VCAL_HUMAN	P19320	homo sapien	1102	139	7.7	824	2	Q912B6	Q912b6	pleurodeles
1030	142.5	7.9	956	1	UNSD_MOUSE	Q8kl52	mus musculus	1103	139	7.7	976	2	Q9W755	Q9w755	brachydanio
1031	142.5	7.9	1019	2	Q8DVR8	Q8dvr8	fugu rubrip	1104	138.5	7.7	313	2	Q8UW13	Q8uw13	lapemis har
1032	142.5	7.9	1052	2	Q9VUC8	Q9vuc8	drosophila	1105	138.5	7.7	360	2	Q8N732	Q8n732	homo sapien
1033	142	7.9	344	2	Q8WR42	Q8wr42	caenorhabdi	1106	138.5	7.7	377	2	Q9VQY0	Q9vqy0	drosophila
1034	142	7.9	345	2	Q8MPV0	Q8mpv0	caenorhabdi	1107	138.5	7.7	413	2	Q26438	Q26438	hyalophora
1035	142	7.9	494	2	Q9ESC6	Q9esc6	mus musculus	1108	138.5	7.7	419	2	Q96QL5	Q96ql5	homo sapien
1036	142	7.9	505	2	Q9U965	Q9u965	geodia cydo	1109	138.5	7.7	719	2	Q9U4G1	Q9u4g1	drosophila
1037	142	7.9	806	1	CEX2_CHICK	P18460	gallus gall	1110	138.5	7.7	1896	2	Q91AJ1	Q91aj1	xenopus lae
1038	142	7.9	1252	2	Q9EQS9	Q9eqs9	mus musculus	1111	138	7.6	313	2	Q9U964	Q9u964	geodia cydo
1039	142	7.9	1253	2	Q9EQS8	Q9eqs8	mus musculus	1112	138	7.6	515	1	PVR1_PIG	Q9gl76	sus scrofa
1040	141.5	7.8	324	2	Q9UPK9	Q9upk9	homo sapien	1113	138	7.6	767	2	Q86YC7	Q86yc7	homo sapien
1041	141.5	7.8	333	2	Q75238	Q75238	homo sapien	1114	138	7.6	1087	1	PGDS_XENLA	P26619	xenopus lae
1042	141.5	7.8	881	2	Q965M2	Q965m2	caenorhabdi	1115	137.5	7.6	357	2	Q63238	Q63238	rattus norv
1043	141.5	7.8	953	1	UNSD_HUMAN	Q6uxz4	homo sapien	1116	137.5	7.6	385	2	Q9VQX8	Q9vqx8	drosophila
1044	141.5	7.8	1007	1	ROB4_HUMAN	Q8wz75	homo sapien	1117	137.5	7.6	413	1	HEMO_HYACE	P25033	hyalophora
1045	141.5	7.8	1227	2	Q21038	Q21038	caenorhabdi	1118	137.5	7.6	419	1	PSG4_HUMAN	Q00888	homo sapien
1046	141.5	7.8	1447	2	Q16779	Q16779	caenorhabdi	1119	137.5	7.6	428	2	Q9BRW2	Q9brw2	homo sapien
1047	141.5	7.8	2000	2	Q97791	Q97791	oryctolagus	1120	137.5	7.6	463	2	Q66J72	Q66j72	xenopus lae
1048	141	7.8	276	2	Q6P0R7	Q6p0r7	brachydanio	1121	137.5	7.6	740	1	PEC1_PIG	Q66j72	sus scrofa
1049	141	7.8	338	2	Q6DHD4	Q6dhd4	brachydanio	1122	137.5	7.6	977	2	Q98SU4	Q98su4	danio albol
1050	141	7.8	432	2	Q6DDE7	Q6dde7	xenopus lae	1123	137.5	7.6	1040	2	Q8NHN2	Q8nhn2	homo sapien
1051	141	7.8	456	2	Q7PUM9	Q7pum9	anopheles g	1124	137.5	7.6	1379	2	P79701	P79701	coturnix co
1052	141	7.8	626	2	Q6DCH3	Q6dch3	xenopus lae	1125	137	7.6	366	2	Q6NVZ3	Q6nvz3	homo sapien
1053	141	7.8	815	2	Q8AYP3	Q8ayp3	brachydanio	1126	137	7.6	420	2	Q68DM9	Q68dm9	homo sapien

835	155	8.6	707	2	Q7PMJ1	Q7pwj1 anopheles g	908	149.5	8.3	360	2	Q8BJ10	Q8bj10 mus musculus
836	155	8.6	819	1	FCR1_CHICK	P21804 gallus gall	909	149.5	8.3	739	1	VCA1_RAT	P29534 rattus norv
837	155	8.6	977	2	Q6RD9	Q6rd9 homo sapien	910	149.5	8.3	835	2	Q805B9	Q805b9 brachydanio
838	155	8.6	1363	1	VGR3_MOUSE	P35917 mus musculus	911	149.5	8.3	1073	2	Q9W1T8	Q9w1t8 drosophila
839	155	8.6	1367	1	VGR2_MOUSE	P35918 mus musculus	912	149.5	8.3	1250	2	Q8TDX8	Q8tdx8 homo sapien
840	154.5	8.6	602	1	NRG1_CHICK	Q55199 gallus gall	913	149.5	8.3	1501	2	Q9QW00	Q9qw00 rattus norv
841	154.5	8.6	1897	1	PTPF_HUMAN	P10586 homo sapien	914	149.5	8.3	1863	2	Q64605	Q64605 rattus norv
842	154.5	8.6	1898	2	Q86WS0	Q86ws0 homo sapien	915	149	8.3	335	2	Q75237	Q75237 homo sapien
843	154	8.5	549	2	Q9D006	Q9d006 mus musculus	916	149	8.3	372	2	Q8K1G0	Q8k1g0 rattus norv
844	154	8.5	606	2	Q9ESS7	Q9ess7 mus musculus	917	149	8.3	373	2	Q8R373	Q8r373 mus musculus
845	154	8.5	624	2	Q9ESS6	Q9ess6 rattus norv	918	149	8.3	388	2	Q9Z151	Q9z151 mus musculus
846	154	8.5	648	2	Q9EPF1	Q9epf1 mus musculus	919	149	8.3	570	2	Q6GLY1	Q6gly1 xenopus lae
847	154	8.5	648	2	Q8R2Y2	Q8r2y2 mus musculus	920	149	8.3	1894	2	Q64487	Q64487 mus musculus
848	154	8.5	686	1	IFL2_HUMAN	Q9np60 h x-linked	921	148.5	8.2	220	2	Q7PX67	Q7px67 anopheles g
849	154	8.5	816	2	Q86PM4	Q86pm4 hydra atten	922	148.5	8.2	289	2	Q7ZWT0	Q7zwt0 xenopus lae
850	154	8.5	1348	1	VGR2_COTJA	P52583 coturnix co	923	148.5	8.2	476	2	Q7ZXJ8	Q7zxj8 xenopus lae
851	153.5	8.5	280	2	Q93350	Q93350 caenorhabdi	924	148.5	8.2	521	1	C166_CANFA	Q46634 canis famli
852	153.5	8.5	1173	2	Q6NR54	Q6nr54 drosophila	925	148.5	8.2	536	2	Q9GV82	Q9gv82 drosophila
853	153.5	8.5	2217	2	Q8AV57	Q8av57 gallus gall	926	148.5	8.2	588	1	C166_CHICK	P42292 gallus gall
854	153.5	8.5	6048	2	Q7JN85	Q7jn85 caenorhabdi	927	148.5	8.2	673	2	Q6MZW2	Q6mzw2 homo sapien
855	153	8.5	307	2	Q7PCU3	Q7pcu3 anopheles g	928	148.5	8.2	821	2	Q9VH44	Q9vh44 xenopus lae
856	153	8.5	1348	2	Q67TM1	Q67tm1 gallus gall	929	148.5	8.2	1173	2	Q9V7J8	Q9v7j8 drosophila
857	153	8.5	1788	2	Q9IAJ0	Q9iaj0 xenopus lae	930	148.5	8.2	1501	2	Q7TTI7	Q7tti7 mus musculus
858	153	8.5	1912	1	PTPD_HUMAN	P23468 homo sapien	931	148.5	8.2	1502	2	Q9UM81	Q9um81 homo sapien
859	152.5	8.4	347	2	Q6PJS2	Q6pjs2 homo sapien	932	148.5	8.2	1887	2	Q9QW67	Q9qw67 rattus norv
860	152.5	8.4	509	2	Q9EQY5	Q9eqy5 m mman-g pr	933	148.5	8.2	1904	2	Q64699	Q64699 mus musculus
861	152.5	8.4	519	1	ECTO_RAT	P16573 rattus norv	934	148	8.2	622	2	Q9JKB2	Q9jkb2 mus musculus
862	152.5	8.4	1802	2	Q28633	Q28633 oryctolagus	935	148	8.2	694	2	Q8SWT7	Q8swt7 drosophila
863	152.5	8.4	7105	2	Q7PXM9	Q7pxm9 anopheles g	936	148	8.2	697	2	Q8TC35	Q8tc35 homo sapien
864	152	8.4	247	2	Q7FVN3	Q7fvm3 anopheles g	937	148	8.2	709	2	Q8IXC7	Q8ixc7 homo sapien
865	152	8.4	636	2	Q22040	Q22040 caenorhabdi	938	147.5	8.2	229	2	Q7PVL3	Q7pvl3 anopheles g
866	152	8.4	687	2	Q9JJO8	Q9jj08 rattus norv	939	147.5	8.2	318	2	Q91664	Q91664 xenopus lae
867	152	8.4	783	2	Q86T42	Q86t42 homo sapien	940	147.5	8.2	331	2	Q63239	Q63239 rattus norv
868	152	8.4	810	2	Q7PUH1	Q7puh1 anopheles g	941	147.5	8.2	403	1	RAGE_MOUSE	Q62151 mus musculus
869	152	8.4	880	1	TYO3_RAT	P55146 rattus norv	942	147.5	8.2	446	2	Q63237	Q63237 rattus norv
870	152	8.4	1024	2	Q63HJ3	Q63hj3 homo sapien	943	147.5	8.2	573	2	Q8GN50	Q8gn50 xenopus lae
871	152	8.4	1092	2	Q13ZT0	Q13zt0 rattus norv	944	147.5	8.2	786	2	Q78E87	Q78e87 mus musculus
872	152	8.4	1141	1	MYPS_HUMAN	Q00872 homo sapien	945	147.5	8.2	1499	2	Q90815	Q90815 gallus gall
873	152	8.4	1148	2	Q8N312	Q8n312 homo sapien	946	147	8.1	402	2	Q35444	Q35444 mus musculus
874	152	8.4	1148	2	Q8N3R4	Q8n3r4 homo sapien	947	147	8.1	549	2	Q9NQS3	Q9nqs3 homo sapien
875	152	8.4	1148	2	Q86T39	Q86t39 homo sapien	948	147	8.1	739	1	PEC1_BOVIN	P51866 bos taurus
876	152	8.4	1171	2	Q86TA8	Q86ta8 homo sapien	949	147	8.1	1044	2	Q961W3	Q961w3 homo sapien
877	152	8.4	1171	2	Q86TC8	Q86tc8 homo sapien	950	147	8.1	1237	2	Q75147	Q75147 homo sapien
878	152	8.4	1343	1	VGR2_RAT	Q08775 rattus norv	951	147	8.1	1252	2	Q9JLI1	Q9jli1 mus musculus
879	152	8.4	1363	2	Q91ZT1	Q91zt1 rattus norv	952	146.5	8.1	275	2	Q7PVM4	Q7pvm4 anopheles g
880	151.5	8.4	228	2	Q7PVK5	Q7pvk5 anopheles g	953	146.5	8.1	291	2	Q6S8Q7	Q6s8q7 homo sapien
881	151.5	8.4	229	2	Q7PUC4	Q7puc4 anopheles g	954	146.5	8.1	326	2	Q8NC17	Q8nc17 homo sapien
882	151.5	8.4	344	1	CEA6_HUMAN	P40199 homo sapien	955	146.5	8.1	468	2	Q9XY08	Q9xy08 bombyx mori
883	151.5	8.4	344	2	Q13774	Q13774 homo sapien	956	146.5	8.1	484	2	Q99JQ8	Q99jq8 mus musculus
884	151.5	8.4	564	2	Q7ZU00	Q7zu00 brachydanio	957	146.5	8.1	606	2	Q9ESS8	Q9ess8 rattus norv
885	151.5	8.4	847	2	Q8BFR2	Q8bfr2 m mus musculus	958	146.5	8.1	648	2	Q9EPF2	Q9epf2 rattus norv
886	151.5	8.4	847	2	Q8C4T3	Q8c4t3 mus musculus	959	146.5	8.1	773	2	Q9NSW7	Q9nsw7 homo sapien
887	151.5	8.4	948	2	Q9TID7	Q9ttid7 trichosurus	960	146.5	8.1	847	2	Q8N475	Q8n475 homo sapien
888	151.5	8.4	1898	2	Q9EQI7	Q9eqi7 mus musculus	961	146.5	8.1	850	2	Q9ULF7	Q9ulf7 homo sapien
889	151	8.4	413	2	Q699P0	Q699p0 antheraea p	962	146.5	8.1	1280	2	Q9EPX2	Q9epx2 mus musculus
890	151	8.4	1156	2	Q676C3	Q676c3 oikopleura	963	146	8.1	309	2	Q7QFT7	Q7qft7 anopheles g
891	150.5	8.3	422	2	Q7RTV9	Q7rtv9 homo sapien	964	146	8.1	486	2	Q8CGH8	Q8cgh8 mus musculus
892	150.5	8.3	437	2	Q9NFK6	Q9nf56 homo sapien	965	146	8.1	549	2	Q9JLB9	Q9jlb9 mus musculus
893	150.5	8.3	509	2	Q91YK7	Q91yk7 mus musculus	966	146	8.1	738	2	P79390	P79390 bos primige
894	150.5	8.3	510	2	Q96K15	Q96k15 homo sapien	967	146	8.1	782	2	Q61563	Q61563 mus musculus
895	150.5	8.3	510	2	Q96N78	Q96ny8 homo sapien	968	146	8.1	790	2	Q8C4N3	Q8c4n3 mus musculus
896	150.5	8.3	824	2	Q90749	Q90749 gallus gall	969	146	8.1	827	1	TRKC_CHICK	Q91044 gallus gall
897	150.5	8.3	888	2	Q7ZWM9	Q7zwm9 xenopus lae	970	146	8.1	1087	2	Q7ZV71	Q7zv71 xenopus lae
898	150.5	8.3	961	1	ROB4_RAT	Q8ow87 rattus norv	971	146	8.1	1088	1	FGDS_RAT	P20786 rattus norv
899	150.5	8.3	1298	1	VGR3_HUMAN	P35916 homo sapien	972	146	8.1	1089	1	FGDS_MOUSE	P26618 mus musculus
900	150.5	8.3	1298	2	Q86W08	Q86w08 homo sapien	973	146	8.1	1089	2	Q7TSJ3	Q7tsj3 mus musculus
901	150.5	8.3	1363	2	Q86W07	Q86w07 homo sapien	974	145.5	8.1	292	2	Q66172	Q66172 brachydanio
902	150	8.3	343	2	Q7TP22	Q7tp22 rattus norv	975	145.5	8.1	504	2	Q6NNA1	Q6nna1 drosophila
903	150	8.3	686	1	IFL2_MOUSE	Q9er56 mus musculus	976	145.5	8.1	508	2	Q9VGD2	Q9vgd2 drosophila
904	150	8.3	711	2	Q24205	Q24205 drosophila	977	145.5	8.1	520	2	Q9Z5P2	Q9z5p2 mus musculus
905	150	8.3	977	2	Q6NXV8	Q6nxv8 mus musculus	978	145.5	8.1	664	2	Q9VGD3	Q9vgd3 drosophila
906	150	8.3	1171	2	Q86T48	Q86t48 homo sapien	979	145.5	8.1	739	1	VCA1_MOUSE	P29533 mus musculus
907	149.5	8.3	349	1	CEA8_HUMAN	P31997 homo sapien	980	145.5	8.1	739	2	Q91X98	Q91x98 mus musculus

689	165.5	9.2	646	1	MUL8_HUMAN	P43121	homo sapien	762	160.5	8.9	980	1	KFMS_FELCA	P13369	felis silve
690	165.5	9.2	1023	2	Q9ULI7	Q9uli7	homo sapien	763	160	8.9	319	1	A33_HUMAN	Q9795	homo sapien
691	165.5	9.2	1193	2	Q9VQW1	Q9vqw1	drosophila	764	160	8.9	485	2	Q801W5	Q801w5	brachydanio
692	165	9.1	584	2	Q9Y3Y8	Q9y3y8	homo sapien	765	160	8.9	544	2	Q7ZZ85	Q7zz85	brachydanio
693	165	9.1	822	1	FGR1_MOUSE	P15092	mus musculus	766	160	8.9	564	1	C166_BRARE	Q90460	brachydanio
694	165	9.1	822	1	FGR1_RAT	Q04589	rattus norv	767	160	8.9	564	2	Q81QX4	Q61qx4	brachydanio
695	165	9.1	822	2	Q60818	Q60818	rattus norv	768	160	8.9	640	2	Q8BSM2	Q8bsm2	mus musculus
696	165	9.1	998	2	Q9W4Y6	Q9w4y6	drosophila	769	160	8.9	822	1	Q8BSM2	Q8bsm2	mus musculus
697	165	9.1	1014	2	Q8NFA6	Q8nfa6	homo sapien	770	160	8.9	1144	2	Q818100	P11362	homo sapien
698	165	9.1	2222	2	Q97394	Q97394	drosophila	771	160	8.9	1437	2	Q44329	Q18100	caenorhabdi
699	165	9.1	2230	2	Q86BQ7	Q86bq7	drosophila	772	160	8.9	1437	2	Q44329	Q18100	caenorhabdi
700	164.5	9.1	438	2	Q920C3	Q920c3	mus musculus	773	159.5	8.8	6839	2	Q23550	Q23550	caenorhabdi
701	164.5	9.1	583	1	C166_HUMAN	Q13740	homo sapien	774	159.5	8.8	570	2	Q8NCE6	Q8nce6	homo sapien
702	164.5	9.1	583	1	C166_RAT	Q35112	rattus norv	775	159.5	8.8	585	2	Q80Y09	Q6uy09	homo sapien
703	164.5	9.1	639	2	Q96P30	Q96p30	homo sapien	776	159	8.8	226	2	Q7P174	Q97174	drosophila
704	164.5	9.1	822	2	Q61674	Q61674	drosophila	777	159	8.8	925	2	Q7P174	Q97174	drosophila
705	164.5	9.1	822	2	Q9V6T1	Q9v6t1	drosophila	778	159	8.8	816	2	Q91285	Q91285	pleurodeles
706	164.5	9.1	1247	2	Q700S6	Q7q0s6	anopheles g	779	158.5	8.8	1948	1	PTNS_HUMAN	Q13332	homo sapien
707	164	9.1	310	2	Q68FQ2	Q68fq2	rattus norv	780	158.5	8.8	388	1	BASI_CHICK	P17790	gallus gall
708	164	9.1	310	2	Q9D1M9	Q9dim9	mus musculus	781	158.5	8.8	912	1	ICAS_RABIT	Q2730	oryctolagus
709	164	9.1	310	2	Q9D8B7	Q9d8b7	mus musculus	782	158.5	8.8	1199	2	Q21041	Q21041	caenorhabdi
710	164	9.1	310	2	Q9EPK4	Q9epk4	m junctiona	783	158.5	8.8	1215	2	Q7KTI7	Q7kti7	drosophila
711	164	9.1	628	1	LU_HUMAN	P50895	homo sapien	784	158.5	8.8	1461	2	Q8T9F6	Q8t9f6	drosophila
712	164	9.1	628	2	Q85VC7	Q86vc7	homo sapien	785	158.5	8.8	1474	2	Q8T4M0	Q8t4m0	drosophila
713	164	9.1	812	2	Q8N6I2	Q8n6i2	homo sapien	786	158.5	8.8	1503	2	Q8T18	Q8t18	drosophila
714	164	9.1	820	2	Q8CIM9	Q8cim9	mus musculus	787	158.5	8.8	1509	2	Q81PG1	Q81pg1	drosophila
715	164	9.1	924	2	Q8TAM9	Q8tam9	homo sapien	788	158.5	8.8	242	2	Q7Q1Q0	Q7q1q0	drosophila
716	164	9.1	998	2	Q95R27	Q95r27	drosophila	789	158	8.7	293	2	Q7QC80	Q7qc80	anopheles g
717	164	9.1	1311	2	Q961K8	Q961k8	drosophila	790	158	8.7	361	2	Q61565	Q61565	mus musculus
718	164	9.1	1394	2	Q62PP2	Q62pp2	mus musculus	791	158	8.7	361	2	Q9QW79	Q9qw79	mus sp. . f
719	164	9.1	2176	2	Q6V4S5	Q6v4s5	mus musculus	792	158	8.7	697	2	Q9QV77	Q9qv77	anopheles g
720	163.5	9.1	483	2	Q9DBP8	Q9dbp8	mus musculus	793	158	8.7	822	2	Q9QV77	Q9qv77	rattus sp.
721	163.5	9.1	508	2	Q8CED8	Q8ced8	mus musculus	794	157.5	8.7	346	2	Q9CTL3	Q9ctl3	mus musculus
722	163.5	9.1	508	2	Q8R007	Q8r007	mus musculus	795	157.5	8.7	441	2	Q8C139	Q8c139	mus musculus
723	163.5	9.1	513	2	Q9D6N4	Q9d6n4	mus musculus	796	157.5	8.7	496	2	Q9TIF9	Q9tif9	mus musculus
724	163.5	9.1	646	2	Q6PBR3	Q6pbr3	homo sapien	797	157.5	8.7	531	2	Q7QEY7	Q7qey7	anopheles g
725	163.5	9.1	1596	2	Q9HCL6	Q9hcl6	homo sapien	798	157.5	8.7	583	1	C166_MOUSE	Q61490	mus musculus
726	163	9.0	357	2	Q18872	Q18872	homo sapien	799	157.5	8.7	697	1	SILA_HUMAN	Q961c7	homo sapien
727	163	9.0	924	1	ICAS_HUMAN	Q9umf0	homo sapien	800	157.5	8.7	939	2	Q967X6	Q967x6	drosophila
728	162.5	9.0	332	2	Q684Q2	Q684q2	mus musculus	801	157.5	8.7	939	2	Q9VB35	Q9vb35	drosophila
729	162.5	9.0	353	2	Q86XY3	Q86xy3	homo sapien	802	157.5	8.7	978	1	KFMS_FSVMD	P00545	feline sarc
730	162.5	9.0	508	2	Q961A5	Q961a5	homo sapien	803	157.5	8.7	1052	2	Q7PMY4	Q7pmY4	anopheles g
731	162.5	9.0	605	2	Q6GNL9	Q6gnl9	xenopus lae	804	157.5	8.7	1503	2	Q8T4L8	Q8t4l8	drosophila
732	162.5	9.0	628	2	Q9NMZ08	Q9nmz08	bos taurus	805	157	8.7	298	1	JAM1_BOVIN	Q9xt56	bos taurus
733	162.5	9.0	1509	2	Q95P10	Q95p10	drosophila	806	157	8.7	299	1	JAM1_HUMAN	Q975m19	homo sapien
734	162.5	9.0	1535	2	Q23991	Q23991	drosophila	807	157	8.7	383	2	Q75ML9	Q75ml9	homo sapien
735	162	9.0	773	2	Q7QBL9	Q7qbl9	anopheles g	808	157	8.7	446	2	Q63236	Q63236	rattus norv
736	162	9.0	1304	2	Q9VBE5	Q9vbe5	drosophila	809	157	8.7	641	2	Q86SD2	Q86sd2	ciona intes
737	162	9.0	4824	2	Q95YI1	Q95ym1	procambarus	810	157	8.7	734	2	Q96LA4	Q96la4	homo sapien
738	161.5	8.9	350	2	Q9VUF7	Q9vuf7	drosophila	811	157	8.7	734	2	Q96P31	Q96p31	homo sapien
739	161.5	8.9	402	2	Q9NAR0	Q9nar0	caenorhabdi	812	157	8.7	742	2	Q8N6S2	Q8n6s2	homo sapien
740	161.5	8.9	638	2	Q7Q766	Q7q766	anopheles g	813	156.5	8.7	416	1	RAGE_BOVIN	Q28173	bos taurus
741	161.5	8.9	650	2	Q7QK22	Q7qk22	bos taurus	814	156.5	8.7	799	2	Q8C3V5	Q8c3v5	mus musculus
742	161.5	8.9	739	2	Q9GKR3	Q9gkr3	bos taurus	815	156.5	8.7	799	2	Q8CIB8	Q8cib8	mus musculus
743	161.5	8.9	802	2	Q42127	Q42127	xenopus lae	816	156.5	8.7	811	2	Q9YH43	Q9yh43	xenopus lae
744	161.5	8.9	2325	2	Q9N3X8	Q9n3x8	caenorhabdi	817	156	8.6	525	2	Q7QJK5	Q7qjk5	anopheles g
745	161.5	8.9	2935	2	Q7Z1Y4	Q7z1y4	drosophila	818	156	8.6	692	2	Q800Y9	Q800y9	brachydanio
746	161.5	8.9	2946	2	Q9W053	Q9w053	drosophila	819	156	8.6	740	2	Q96P29	Q96p29	homo sapien
747	161	8.9	298	2	Q8INK5	Q8ink5	drosophila	820	156	8.6	756	2	Q800Z0	Q800z0	brachydanio
748	161	8.9	309	2	Q96FL1	Q96fl1	homo sapien	821	156	8.6	977	1	KFMS_MOUSE	P09581	mus musculus
749	161	8.9	310	1	JAM3_HUMAN	Q9bx67	homo sapien	822	156	8.6	978	1	KFMS_RAT	Q00495	rattus norv
750	161	8.9	336	2	Q961T8	Q961t8	drosophila	823	156	8.6	1501	2	Q7KUK9	Q7kuk9	drosophila
751	161	8.9	461	2	Q13854	Q13854	homo sapien	824	156	8.6	1860	2	Q7PQF4	Q7pqf4	anopheles g
752	161	8.9	527	2	Q62TR2	Q62tr2	homo sapien	825	156	8.6	7158	2	Q23551	Q23551	caenorhabdi
753	161	8.9	538	2	Q29123	Q29123	sus scrofa	826	155.5	8.6	761	2	Q95LQ2	Q95lq2	macaca fasc
754	161	8.9	605	2	Q8TBU0	Q8tbu0	homo sapien	827	155.5	8.6	880	1	TYO3_MOUSE	P55144	mus musculus
755	161	8.9	693	2	Q8QFHL3	Q8qfhl3	gallus gall	828	155.5	8.6	880	2	Q6NZM6	Q6nzm6	mus musculus
756	161	8.9	1327	2	Q8QHL3	Q8qhl3	gallus gall	829	155	8.6	373	2	Q9H6B4	Q9h6b4	homo sapien
757	161	8.9	1345	2	Q8VCD0	Q8vcd0	mus musculus	830	155	8.6	454	2	Q91W54	Q91w54	mus musculus
758	161	8.9	2541	2	Q19663	Q19663	caenorhabdi	831	155	8.6	458	2	Q61351	Q61351	mus musculus
759	160.5	8.9	422	2	Q86CY9	Q86cy9	helicoverpa	832	155	8.6	521	1	CEA1_MOUSE	P31809	mus musculus
760	160.5	8.9	646	2	Q95812	Q95812	homo sapien	833	155	8.6	521	2	Q925P3	Q925p3	mus musculus
761	160.5	8.9	646	2	Q8NHN8	Q8nhn8	homo sapien	834	155	8.6	521	2	Q61352	Q61352	mus musculus

543	179	9.9	300	1	JAM1 MOUSE	O88792	mus musculus	616	172	9.5	287	2	Q13984	Q13984 homo sapien
544	179	9.9	300	2	O8VC39	O8VC39	mus musculus	617	172	9.5	319	1	A33 MOUSE	O9jka5 mus musculus
545	179	9.9	626	1	MAG MOUSE	P20917	mus musculus	618	172	9.5	371	2	O7Q127	O7ql27 anopheles g
546	179	9.9	814	2	O81VU1	O81vul1	homo sapien	619	172	9.5	1045	2	O86T37	O86t37 homo sapien
547	179	9.9	917	1	1CA5 MOUSE	Q60625	mus musculus	620	172	9.5	1320	2	O96KFS	O96kfs homo sapien
548	179	9.9	1019	2	O8BJK6	O8bjk6	mus musculus	621	172	9.5	1320	2	O86TC9	O86tc9 homo sapien
549	178.5	9.9	1234	1	1NPN RAT	O91044	rattus norv	622	172	9.5	2403	2	O8MLD5	O8mld5 drosophila
550	178.5	9.9	1252	2	O9JIX2	O9jix2	rattus norv	623	172	9.5	4736	2	O7YT99	O7yt99 mytilus gal
551	178	9.9	310	2	O7QK35	O7qk35	anopheles g	624	172	9.5	7210	2	O9V7G8	O9v7g8 drosophila
552	178	9.9	379	2	O9CWN1	O9cwn1	mus musculus	625	171.5	9.5	283	2	O9VT76	O9vt76 drosophila
553	178	9.9	413	1	HEMO MANSE	P31398	manduca sex	626	171.5	9.5	307	2	O94431	O94431 ciona intes
554	178	9.9	492	2	O9ET54	O9et54	mus musculus	627	171.5	9.5	1338	1	VGR1 HUMAN	P17948 h vascular
555	178	9.9	853	2	O6DFX7	O6dfx7	mus musculus	628	171.5	9.5	2772	2	O9VAV4	O9vav4 drosophila
556	178	9.9	1073	2	O9TXI8	O9txi8	caenorhabdi	629	171.5	9.5	2894	2	O7KRX2	O7kxr2 drosophila
557	178	9.9	1081	2	O69ZT7	O69zt7	mus musculus	630	171.5	9.5	26926	2	O10466	O10466 homo sapien
558	177.5	9.8	344	2	O9VY33	O9vy33	drosophila	631	171	9.5	373	2	O7KIF5	O7kyps homo sapien
559	177.5	9.8	457	2	O96OD1	O96od1	drosophila	632	171	9.5	464	2	O16170	O16170 homo sapien
560	177.5	9.8	583	1	C166 BOVIN	O9bh13	bos taurus	633	171	9.5	468	2	O96CA7	O96ca7 homo sapien
561	177.5	9.8	717	2	O7PUQ1	O7puq1	anopheles g	634	171	9.5	526	1	CEA1 HUMAN	P13688 homo sapien
562	177.5	9.8	796	2	O91287	O91287	pleurodeles	635	171	9.5	534	2	O86SE4	O86se4 homo sapien
563	177.5	9.8	1249	2	O7TMZ9	O7tmz9	rattus norv	636	171	9.5	764	2	O8MQQ1	O8mqq1 drosophila
564	177.5	9.8	1527	2	O9VZZ4	O9vzz4	drosophila	637	171	9.5	810	2	O9PS96	O9ps96 xenopus lae
565	177.5	9.8	1933	2	O6V3A4	O6v3a4	mus musculus	638	171	9.5	1255	2	O7Z3Z9	O7z3z9 homo sapien
566	177	9.8	376	2	O9OZ71	O9oz71	brachydanio	639	171	9.5	1257	1	CAML HUMAN	P32004 homo sapien
567	177	9.8	404	2	O9OZ71	O9y3e9	homo sapien	640	171	9.5	2224	2	O9ULM1	O9ulm1 drosophila
568	177	9.8	577	2	O8OY42	O8oy42	mus musculus	641	171	9.5	26926	2	O8WZB3	O8wzb3 homo sapien
569	177	9.8	1331	2	O7Q623	O7q623	anopheles g	642	170.5	9.4	370	2	O8O0Y8	O8o0y8 brachydanio
570	177	9.8	2242	2	O7P2P9	O7p2p9	homo sapien	643	170.5	9.4	501	2	O6Q147	O6q147 bos taurus
571	177	9.8	3625	2	O86GD6	O86gd6	procambarus	644	170.5	9.4	521	1	C166 RABIT	O46651 oryctolagus
572	176.5	9.8	830	2	O86PJI	O86pji	homo sapien	645	170.5	9.4	540	2	O8N0Z9	O8n0z9 homo sapien
573	176.5	9.8	510	2	O7L3E0	O7l3e0	homo sapien	646	170.5	9.4	591	2	O6NP04	O6np04 drosophila
574	176.5	9.8	686	1	S1LB HUMAN	O96rl6	homo sapien	647	170	9.4	291	2	O66J15	O66j15 xenopus tro
575	176.5	9.8	772	2	O9Y2J6	O9y2j6	homo sapien	648	170	9.4	300	2	O9JHY1	O9jhy1 rattus norv
576	176.5	9.8	1106	2	O8WX93	O8wx93	homo sapien	649	170	9.4	812	1	FGRL XENLA	P22182 xenopus lae
577	176.5	9.8	2169	2	O8AV58	O8av58	gallus gall	650	169.5	9.4	265	2	O7PUD3	O7puu3 anopheles g
578	176.5	9.8	3029	2	O7Q767	O7q767	anopheles g	651	169.5	9.4	351	2	O8JFU3	O8jfu3 brachydanio
579	176	9.7	410	2	O6R319	O6r319	bombyx mand	652	169.5	9.4	351	2	O7SY58	O7sy58 brachydanio
580	176	9.7	577	2	O8D2Z1	O8d2z1	m mus muscu	653	169.5	9.4	402	1	RAGE RAT	O63495 rattus norv
581	176	9.7	964	2	O18382	O18382	caenorhabdi	654	169.5	9.4	402	2	O6MG86	O6mg86 rattus norv
582	175.5	9.7	1196	2	O85210	O85210	caenorhabdi	655	169.5	9.4	960	2	O7PV74	O7pv74 anopheles g
583	175.5	9.7	1227	2	O9B1A2	O9bia2	caenorhabdi	656	169.5	9.4	2200	2	O7YRF6	O7yrf6 canis famli
584	175	9.7	234	2	O81ZQ9	O81zq9	homo sapien	657	169	9.4	764	1	ICCR DROME	O8180 drosophila
585	175	9.7	1391	2	O8N314	O8n314	homo sapien	658	169	9.4	764	2	O9W4U1	O9w4u1 drosophila
586	174.5	9.7	662	2	O7PSS9	O7pss9	anopheles g	659	169	9.4	814	2	O91897	O91897 xenopus lae
587	174	9.6	210	2	O7PVL9	O7pvl9	anopheles g	660	169	9.4	1254	2	O674V1	O674v1 podocoryne
588	174	9.6	534	2	O866T2	O866t2	pan troglod	661	168.5	9.3	800	2	O86LF9	O86lf9 drosophila
589	174	9.6	675	2	O7T0V5	O7t0v5	xenopus lae	662	168.5	9.3	801	2	O86LF8	O86lf8 drosophila
590	174	9.6	736	2	O8MYS2	O8mys2	drosophila	663	168.5	9.3	2159	2	O6PAL2	O6pal2 mus musculus
591	174	9.6	774	2	O9V930	O9v930	drosophila	664	168	9.3	215	2	O9VRL5	O9vrl5 drosophila
592	174	9.6	1255	2	O7YQL7	O7yql7	pongo pygma	665	168	9.3	827	2	O6GNS5	O6gns5 xenopus lae
593	174	9.6	1255	2	O7YQL8	O7yql8	pan troglod	666	168	9.3	2051	2	O44328	O44328 hirudo medi
594	174	9.6	1721	2	O961U1	O961ul1	drosophila	667	167.5	9.3	555	1	C166 CARAU	O90304 carassius a
595	174	9.6	2389	2	O6BEQ6	O6beq6	caenorhabdi	668	167.5	9.3	784	2	O81063	O81063 drosophila
596	174	9.6	3375	1	UN52 CAEEL	O66561	caenorhabdi	669	167.5	9.3	939	2	O9VH85	O9vh85 drosophila
597	174	9.6	4650	2	O15598	O15598	homo sapien	670	167.5	9.3	1019	2	O9Y6L9	O9y6l9 homo sapien
598	174	9.6	6658	2	O76281	O76281	drosophila	671	167.5	9.3	1694	1	SN MOUSE	O62230 mus musculus
599	173.5	9.6	196	2	O7PJY5	O7pjy5	anopheles g	672	167.5	9.3	2776	2	O869A0	O869a0 drosophila
600	173.5	9.6	360	2	O8MR6E	O8mre6	drosophila	673	167.5	9.3	2898	2	O868Z9	O868z9 drosophila
601	173.5	9.6	442	2	O6KAT6	O6kat6	mus musculus	674	167	9.2	376	2	O9QW78	O9qw78 mus sp. . f
602	173.5	9.6	538	2	O9NWO7	O9nwq7	homo sapien	675	167	9.2	489	2	O7PGL7	O7pgl7 anopheles g
603	173.5	9.6	544	2	O6UXI8	O6uxi8	homo sapien	676	167	9.2	551	2	O8MSN7	O8msn7 drosophila
604	173.5	9.6	600	2	O7PN36	O7pn36	anopheles g	677	167	9.2	956	2	O9W4T9	O9w4t9 drosophila
605	173.5	9.6	1021	2	P79757	P79757	gallus gall	678	167	9.2	959	2	O9N9Y9	O9ny9 drosophila
606	173.5	9.6	1235	2	O7Q0S7	O7q0s7	anopheles g	679	167	9.2	1276	2	O90X22	O90x22 brachydanio
607	173.5	9.6	4463	2	O8MLD8	O8mld8	drosophila	680	167	9.2	1356	1	VGR2 HUMAN	P35968 homo sapien
608	173.5	9.6	9270	2	O8MLD9	O8mld9	drosophila	681	167	9.2	2200	1	LAR CAEEL	O9bmn8 caenorhabdi
609	173	9.6	385	2	O3UQF5	O9ugf5	homo sapien	682	166.5	9.2	1506	2	O9V7G6	O9v7g6 drosophila
610	173	9.6	410	2	O6R3M0	O6r3m0	bombyx mori	683	166.5	9.2	4039	2	O7ZZ46	O7zz46 brachydanio
611	173	9.6	410	2	O6R3M2	O6r3m2	bombyx mori	684	166	9.2	576	2	O8MYR8	O8myr8 drosophila
612	173	9.6	410	2	O7YZA7	O7yza7	bombyx mori	685	166	9.2	997	2	O7PXX0	O7pxx0 anopheles g
613	173	9.6	1248	2	O9XT41	O9xt41	cercopithec	686	166	9.2	1232	2	O8TCG8	O8tcg8 homo sapien
614	172.5	9.6	357	2	O8R112	O8r112	mus musculus	687	165.5	9.2	340	2	O9W3N2	O9w3n2 drosophila
615	172.5	9.6	1880	2	O18465	O18465	hirudo medi	688	165.5	9.2	538	2	O28939	O28939 sus scrofa

Q13984	homo sapien
O9jka5	mus musculus
O7ql27	anopheles g
O86t37	homo sapien
O96kfs	homo sapien
O86tc9	homo sapien
O8mld5	drosophila
O7yt99	mytilus gal
O9v7g8	drosophila
O9vt76	drosophila
O94431	ciona intes
P17948	h vascular
O9vav4	drosophila
O7kxr2	drosophila
O10466	homo sapien
O7kyps	homo sapien
O16170	homo sapien
O96ca7	homo sapien
P13688	homo sapien
O86se4	homo sapien
O8mqq1	drosophila
O9ps96	xenopus lae
O7z3z9	homo sapien
P32004	homo sapien
O9ulm1	drosophila
O8wzb3	homo sapien
O8o0y8	brachydanio
O6q147	bos taurus
O46651	oryctolagus
O8n0z9	homo sapien
O6np04	drosophila
O66j15	xenopus tro
O9jhy1	rattus norv
P22182	xenopus lae
O7puu3	anopheles g
O8jfu3	brachydanio
O7sy58	brachydanio
O63495	rattus norv
O6mg86	rattus norv
O7pv74	anopheles g
O7yrf6	canis famli
O8180	drosophila
O9w4u1	drosophila
O91897	xenopus lae
O674v1	podocoryne
O86lf9	drosophila
O86lf8	drosophila
O6pal2	mus musculus
O9vrl5	drosophila
O6gns5	xenopus lae
O44328	hirudo medi
O90304	carassius a
O81063	drosophila
O9vh85	drosophila
O9y6l9	homo sapien
O62230	mus musculus
O869a0	drosophila
O868z9	drosophila
O9qw78	mus sp. . f
O7pgl7	anopheles g
O8msn7	drosophila
O9w4t9	drosophila
O9ny9	drosophila
O90x22	brachydanio
P35968	homo sapien
O9bmn8	caenorhabdi
O9v7g6	drosophila
O7zz46	brachydanio
O8myr8	drosophila
O7pxx0	anopheles g
O8tcg8	homo sapien
O9w3n2	drosophila
O28939	sus scrofa

397	193	10.7	949	2	Q8TGN3	Q8ign3 drosophila	470	186	10.3	708	1	KIR2_HUMAN	Q6uwl6 homo sapien
398	193	10.7	1166	2	Q9QVN4	Q9gnv4 rattus sp.	471	186	10.3	899	2	Q7PQM9	Q7pqm9 anopheles g
399	193	10.7	1508	2	Q6NR34	Q6nr34 drosophila	472	186	10.3	899	2	Q7PQM9	Q7pqm9 anopheles g
400	193	10.7	1508	2	Q9VQY2	Q9vgy2 drosophila	473	186	10.3	2558	2	Q6NR91	Q6nr91 drosophila
401	193	10.7	1531	2	Q967D7	Q967d7 drosophila	474	186	10.3	2558	2	Q7KQP6	Q7kqp6 drosophila
402	193	10.7	2029	1	LAR_DROME	P16221 drosophila	475	185.5	10.3	347	2	Q86SNI	Q86sn1 homo sapien
403	193	10.7	2029	2	Q9WIS8	Q9wis8 drosophila	476	185.5	10.3	404	1	RAGE_HUMAN	Q15109 homo sapien
404	192.5	10.7	1150	2	Q8BS24	Q8bs24 mus musculus	477	185.5	10.3	702	1	CEA5_HUMAN	P05731 homo sapien
405	192.5	10.7	1209	2	P70232	P70232 mus musculus	478	185.5	10.3	702	2	Q8N4D0	Q8n4d0 homo sapien
406	192.5	10.7	1259	2	Q6PGJ3	Q6pgj3 mus musculus	479	185.5	10.3	702	2	Q8MMJ9	Q8mmj9 bombyx mori
407	192.5	10.7	1260	1	CAML_MOUSE	P11627 mus musculus	480	185.5	10.3	3354	2	Q8T101	Q8t101 bombyx mori
408	192.5	10.7	1284	1	NRCA_CHICK	P35331 gallus gall	481	185	10.2	582	2	Q8R4B5	Q8r4b5 mus musculus
409	192	10.6	399	2	Q8N772	Q8n772 homo sapien	482	185	10.2	778	1	KIR3_MOUSE	Q8br86 mus musculus
410	192	10.6	529	2	Q91V87	Q91v87 mus musculus	483	185	10.2	789	1	KIR1_RAT	Q6x936 rattus norv
411	192	10.6	602	2	Q86YJ9	Q86y99 homo sapien	484	185	10.2	1020	2	Q8NHN0	Q8nhn0 homo sapien
412	192	10.6	650	2	Q8NA84	Q8na84 homo sapien	485	185	10.2	1294	2	Q8WZ52	Q8wz52 homo sapien
413	192	10.6	1256	2	Q35158	Q35158 rattus norv	486	185	10.2	1427	2	Q91562	Q91562 xenopus lae
414	192	10.6	1304	1	NRCA_HUMAN	Q92823 homo sapien	487	184.5	10.2	424	2	Q8C6W0	Q8c6w0 mus musculus
415	192	10.6	1378	1	ROB2_HUMAN	Q9hck4 homo sapien	488	184.5	10.2	570	2	Q6GMZ9	Q6gmz9 xenopus lae
416	191.5	10.6	1060	2	Q9QZ13	Q9qzi3 rattus norv	489	184.5	10.2	826	2	Q7Q1P7	Q7qlp7 anopheles g
417	191	10.6	509	2	Q920C2	Q920c2 mus musculus	490	184.5	10.2	3094	2	Q695L1	Q695l1 homo sapien
418	191	10.6	2154	2	Q8WZ51	Q8wz51 homo sapien	491	184	10.2	421	2	Q7PV30	Q7pv30 anopheles g
419	190.5	10.5	388	2	Q8R464	Q8r464 mus musculus	492	184	10.2	421	2	Q7QLK4	Q7qlk4 anopheles g
420	190.5	10.5	1154	2	Q9QVN3	Q9qvn3 rattus sp.	493	184	10.2	474	2	Q7PKE3	Q7pke3 anopheles g
421	190.5	10.5	1194	2	Q6PW35	Q6pw35 rattus norv	494	184	10.2	626	1	MAG_RAT	P07722 rattus norv
422	190.5	10.5	1197	2	Q6PW38	Q6pw38 rattus norv	495	184	10.2	757	1	KIR1_HUMAN	Q96j84 homo sapien
423	190.5	10.5	1198	2	Q6PW37	Q6pw37 rattus norv	496	184	10.2	1033	2	Q24327	Q24327 drosophila
424	190.5	10.5	1206	2	Q6PW36	Q6pw36 rattus norv	497	184	10.2	1033	2	Q9V643	Q9v643 drosophila
425	190.5	10.5	1209	2	Q6PW39	Q6pw39 rattus norv	498	184	10.2	1302	1	VGR2_BRARE	Q8axb3 brachydanio
426	190.5	10.5	1214	1	NRCA_RAT	P97686 rattus norv	499	183.5	10.2	2213	2	Q7Z5N4	Q7z5n4 homo sapien
427	190.5	10.5	1299	2	Q6PW34	Q6pw34 rattus norv	500	183	10.1	1232	2	Q90284	Q90284 carassius a
428	190.5	10.5	1366	1	ROB3_MOUSE	Q9z2i4 mus musculus	501	183	10.1	1328	2	Q21043	Q21043 caenorhabdi
429	190.5	10.5	4001	2	Q9N2P7	Q9n2p7 drosophila	502	183	10.1	4816	2	Q8T103	Q8t103 bombyx mori
430	190.5	10.5	4796	2	Q9N188	Q9n188 drosophila	503	182.5	10.1	260	2	Q9XDX7	Q9xxd7 caenorhabdi
431	190.5	10.5	4796	2	Q9W055	Q9w055 drosophila	504	182.5	10.1	931	2	Q8NF26	Q8nf26 homo sapien
432	190	10.5	345	2	Q811H7	Q811h7 mus musculus	505	182.5	10.1	997	2	Q44087	Q44087 caenorhabdi
433	190	10.5	381	2	Q9Y4A4	Q9y4a4 homo sapien	506	182.5	10.1	1083	2	Q76698	Q76698 caenorhabdi
434	190	10.5	551	2	Q8NHN7	Q8nhn7 homo sapien	507	182.5	10.1	1098	2	Q961D6	Q961d6 drosophila
435	190	10.5	781	2	Q7PX10	Q7pxi0 anopheles g	508	182.5	10.1	1332	2	Q9BN17	Q9bn17 drosophila
436	190	10.5	1406	2	Q9GPP7	Q9gpp7 drosophila	509	182.5	10.1	1332	2	Q9VQW7	Q9vgw7 drosophila
437	190	10.5	1463	2	Q9VQ08	Q9vq08 drosophila	510	182.5	10.1	1336	1	VGR1_RAT	P53767 rattus norv
438	189.5	10.5	433	2	Q9V644	Q9v644 drosophila	511	182.5	10.1	1944	2	Q895L3	Q895l3 brachydanio
439	189.5	10.5	602	2	Q9VFD9	Q9vfd9 drosophila	512	182	10.1	626	1	MAG_HUMAN	P29916 homo sapien
440	189.5	10.5	765	2	Q9BKQ1	Q9bkq1 aplysia cal	513	182	10.1	877	2	Q9GSH3	Q9gsh3 halocynthia
441	189.5	10.5	765	2	Q9TWA4	Q9twa4 aplysia cal	514	182	10.1	2212	2	Q8NHN3	Q8nhn3 homo sapien
442	189.5	10.5	812	2	Q9BKQ0	Q9bkq0 aplysia cal	515	182	10.1	17903	2	Q7RTL4	Q7rtl4 drosophila
443	189.5	10.5	812	2	Q9TWA5	Q9twa5 aplysia cal	516	181.5	10.0	793	2	Q70246	Q70246 mus musculus
444	189.5	10.5	880	2	Q7XPQ8	Q7xpq8 drosophila	517	181.5	10.0	813	2	Q8BQC3	Q8bqc3 mus musculus
445	189.5	10.5	932	2	Q9BKP9	Q9bkp9 aplysia cal	518	181.5	10.0	1125	2	Q7QEC1	Q7qec1 anopheles g
446	189.5	10.5	932	2	Q9TWA6	Q9twa6 aplysia cal	519	181.5	10.0	1197	1	CAML_MOUSE	Q90478 brachydanio
447	189.5	10.5	1280	2	Q90933	Q90933 gallus gall	520	181.5	10.0	1333	1	VGR1_MOUSE	P35969 mus musculus
448	189	10.5	750	2	Q646H5	Q646h5 caenorhabdi	521	181	10.0	885	2	Q8N237	Q8n237 homo sapien
449	188.5	10.4	1032	2	Q8AXZ4	Q8axz4 brachydanio	522	181	10.0	913	2	Q8T3E5	Q8t3e5 caenorhabdi
450	188.5	10.4	1036	2	Q8SWW3	Q8sww3 drosophila	523	181	10.0	928	2	Q19128	Q19128 caenorhabdi
451	188.5	10.4	1390	2	Q9VN14	Q9vn14 drosophila	524	181	10.0	955	2	Q8MQ86	Q8mq86 caenorhabdi
452	188.5	10.4	1842	2	Q81ZY3	Q81zy3 homo sapien	525	181	10.0	1244	2	Q69YJ3	Q69y93 homo sapien
453	188	10.4	529	2	Q7TQM3	Q7tqm3 rattus norv	526	181	10.0	1263	2	Q7Z3B7	Q7z3b7 homo sapien
454	188	10.4	789	1	KIR1_MOUSE	Q7tqm3 rattus norv	527	181	10.0	3198	2	Q9U8G8	Q9u8g8 manduca sex
455	188	10.4	1177	2	Q6GQB1	Q6gqb1 xenopus lae	528	181	10.0	5604	2	Q8WZ53	Q8wz53 homo sapien
456	187.5	10.4	538	2	Q9QYQ7	Q9qyq7 mus musculus	529	180.5	10.0	848	2	Q25198	Q25198 hydra atten
457	187.5	10.4	1250	2	Q88971	Q88971 mus musculus	530	180.5	10.0	1242	1	NPHN_MOUSE	Q9qz87 mus musculus
458	187.5	10.4	1259	1	CAML_RAT	Q05695 rattus norv	531	180.5	10.0	1256	2	Q925S5	Q925s5 mus musculus
459	187.5	10.4	1266	1	NGCA_CHICK	Q03696 gallus gall	532	180.5	10.0	1266	2	Q9ET59	Q9et59 mus musculus
460	187.5	10.4	2419	2	Q7PXZ1	Q7pxz1 anopheles g	533	180.5	10.0	1256	2	Q9JIX1	Q9jix1 mus musculus
461	187	10.4	687	2	Q7ZTN4	Q7ztm4 xenopus lae	534	180.5	10.0	1269	2	Q6U7I5	Q6u7i5 brachydanio
462	187	10.4	778	1	KIR3_HUMAN	Q8izu9 homo sapien	535	180	10.0	413	2	Q27418	Q27418 manduca sex
463	187	10.4	1470	1	ROB2_MOUSE	Q7tpd3 mus musculus	536	180	10.0	609	2	Q7QHA0	Q7qha0 anopheles g
464	187	10.4	2133	2	Q7PQG9	Q7pqg9 anopheles g	537	180	10.0	18412	2	Q7ZZ61	Q7zz61 brachydanio
465	187	10.4	2174	2	Q9GQR0	Q9gqr0 drosophila	538	179.5	9.9	333	2	Q90Z41	Q90z41 gallus gall
466	187	10.4	2995	2	Q696W0	Q696w0 brachydanio	539	179.5	9.9	362	2	Q9JH01	Q9jhq1 rattus norv
467	186.5	10.3	922	2	Q90413	Q90413 brachydanio	540	179.5	9.9	503	2	Q9W259	Q9w259 drosophila
468	186.5	10.3	1264	2	Q14631	Q14631 homo sapien	541	179.5	9.9	804	2	Q800Z1	Q800z1 brachydanio
469	186.5	10.3	1889	2	Q7Q0X2	Q7q0x2 anopheles g	542	179.5	9.9	806	2	Q90Z00	Q90z00 brachydanio

251	215	11.9	789	2	Q7PME2	Q7pme2 anopheles g	324	202	11.2	1269	2	001632	001632 caenorhabdi
252	215	11.9	1419	2	Q8SW3	Q8sw3 brachydanio	325	202	11.2	1273	2	044928	044928 caenorhabdi
253	214.5	11.9	816	2	Q8NFA5	Q8nfa5 homo sapien	326	202	11.2	1409	2	08JI27	08ji27 brachydanio
254	214.5	11.9	1070	2	Q6IQ54	Q6iq54 homo sapien	327	202	11.2	1409	2	Q801M2	Q801m2 brachydanio
255	214.5	11.9	1651	1	ROB1_RAT	O55005 rattus norv	328	202	11.2	1428	2	Q8AY67	Q8ay67 brachydanio
256	214	11.8	240	2	Q7PRJ5	Q7prj5 anopheles g	329	202	11.2	2022	2	Q7KQ55	Q7kq55 drosophila
257	214	11.8	498	2	Q8BRT6	Q8brt6 mus musculu	330	201.5	11.2	388	2	Q8NFZ8	Q8nfz8 homo sapien
258	213.5	11.8	391	2	Q7QJG1	Q7qjg1 anopheles g	331	201.5	11.2	771	2	Q7QEX8	Q7qey8 anopheles g
259	213.5	11.8	398	2	Q8N126	Q8n126 homo sapien	332	201.5	11.2	2008	2	Q3VEJ5	Q3vej5 drosophila
260	213.5	11.8	920	2	Q9F232	Q9f232 homo sapien	333	201.5	11.2	2046	2	Q7KSE9	Q7kse9 drosophila
261	213.5	11.8	1389	2	Q90Z69	Q90z69 brachydanio	334	201.5	11.2	3215	2	Q8IRV7	Q8irv7 drosophila
262	213	11.8	484	2	Q6BE00	Q6be00 xenopus lae	335	201.5	11.2	3262	2	Q3EQJ5	Q3eqj5 mus musculu
263	213	11.8	898	2	Q69Z26	Q69z26 mus musculu	336	201.5	11.2	4117	2	Q8IRV9	Q8irv9 drosophila
264	213	11.8	1134	2	Q71B05	Q71b05 brachydanio	337	201.5	11.2	4179	2	Q9W4V4	Q9w4v4 drosophila
265	212.5	11.8	1264	2	P91767	P91767 manduca sex	338	201.5	11.2	4223	2	Q8MPN3	Q8mpn3 drosophila
266	212	11.7	1026	2	Q6Z845	Q6z845 rattus norv	339	201.5	11.2	4228	2	Q8IRV8	Q8irv8 drosophila
267	212	11.7	1151	2	Q9QVNS	Q9qvn5 rattus sp.	340	201.5	11.2	8647	2	Q7KQP5	Q7kqp5 drosophila
268	211.5	11.7	382	2	Q7QSH7	Q7qsh7 anopheles g	341	201.5	11.2	8930	2	Q7KQP7	Q7kqp7 drosophila
269	211.5	11.7	749	2	Q7Q6H1	Q7q6h1 anopheles g	342	201.5	11.2	8943	2	Q9V4F7	Q9v4f7 drosophila
270	211.5	11.7	873	1	FAS2_DROME	P34082 drosophila	343	201	11.1	487	2	Q7T2H2	Q7t2h2 gallus gall
271	211.5	11.7	1070	1	PRK7_HUMAN	Q13308 homo sapien	344	201	11.1	623	2	Q8BY18	Q8by18 mus musculu
272	211.5	11.7	1102	2	Q923W7	Q923w7 mus musculu	345	201	11.1	688	2	Q80ZE3	Q80ze3 mus musculu
273	211.5	11.7	1109	2	Q8CE91	Q8ce91 mus musculu	346	201	11.1	700	1	KIR2_MOUSE	Q7tcsu7 mus musculu
274	211.5	11.7	1109	2	Q6AZB0	Q6azb0 mus musculu	347	201	11.1	946	2	Q07153	Q07153 torpedo cal
275	211.5	11.7	1110	2	Q8CE73	Q8ce73 mus musculu	348	201	11.1	1709	1	SN_HUMAN	Q9bzz2 homo sapien
276	211.5	11.7	1461	1	NEO1_HUMAN	Q92859 homo sapien	349	201	11.1	1735	2	Q7Q916	Q7q916 anopheles g
277	211.5	11.7	1476	2	Q7QJ29	Q7qj29 anopheles g	350	200.5	11.1	1086	2	Q7QH02	Q7qh02 anopheles g
278	211	11.7	396	2	Q99N28	Q99n28 m nectin-1i	351	200.5	11.1	1271	2	Q6U714	Q6u714 brachydanio
279	211	11.7	6620	2	Q96AA2	Q96aa2 homo sapien	352	200.5	11.1	1447	1	DCC_MOUSE	P70211 mus musculu
280	210	11.6	1561	2	Q924D2	Q924d2 mus musculu	353	200.5	11.1	1493	1	NEO1_MOUSE	P97798 mus musculu
281	210	11.6	1730	2	Q7YRQ7	Q7yrq7 sus scrofa	354	200.5	11.1	5516	2	Q7ZZ48	Q7zz48 brachydanio
282	210	11.6	1914	1	KMLS_HUMAN	O15746 homo sapien	355	199.5	11.0	1445	2	Q63155	Q63155 rattus norv
283	210	11.6	1914	2	Q7Z4J0	Q7z4j0 homo sapien	356	199.5	11.0	1465	2	Q7TQ55	Q7tqg5 mus musculu
284	210	11.6	1940	2	Q6PDN3	Q6pdn3 mus musculu	357	199	11.0	440	2	Q6ZMD4	Q6zmd4 homo sapien
285	209	11.6	504	2	Q8N441	Q8n441 homo sapien	358	199	11.0	940	2	Q8NFA7	Q8nfa7 homo sapien
286	209	11.6	504	2	Q8NFA7	Q8nfa7 homo sapien	359	199	11.0	1241	1	NPHN_HUMAN	Q60500 homo sapien
287	209	11.6	1030	2	Q8NFA8	Q8nfa8 homo sapien	360	199	11.0	1513	2	Q90Z70	Q90z70 brachydanio
288	209	11.6	2222	2	Q7QEG7	Q7qeg7 anopheles g	361	199	11.0	1723	2	Q8CHB2	Q8chb2 mus musculu
289	208.5	11.5	1028	2	Q7Q409	Q7q409 mus musculu	362	198.5	11.0	931	2	Q8KAM5	Q8kam5 mus musculu
290	208.5	11.5	1651	1	ROB1_HUMAN	Q9Y6N7 homo sapien	363	198.5	11.0	2053	2	Q8IZY4	Q8izy4 homo sapien
291	208	11.5	1155	2	Q7Q3K8	Q7q3k8 anopheles g	364	198	11.0	437	2	Q86YV1	Q86yv1 homo sapien
292	207.5	11.5	329	2	Q8N225	Q8n225 homo sapien	365	198	11.0	662	2	Q60926	Q60926 homo sapien
293	207.5	11.5	1643	2	Q7QGT8	Q7qgt8 anopheles g	366	198	11.0	847	1	CD22_HUMAN	P20273 homo sapien
294	207	11.5	600	2	Q8N7W7	Q8n7w7 homo sapien	367	198	11.0	907	2	Q9NEG0	Q9neg0 drosophila
295	206.5	11.4	915	2	Q8R4B3	Q8r4b3 mus musculu	368	198	11.0	1240	1	NFAS_RAT	P97685 rattus norv
296	206.5	11.4	2016	2	Q9NBA1	Q9nba1 drosophila	369	197.5	10.9	1164	2	Q66MNS	Q66mn5 drosophila
297	206	11.4	1187	2	Q8WR45	Q8wr45 caenorhabdi	370	197.5	10.9	1228	2	Q8MRA3	Q8mra3 drosophila
298	205.5	11.4	1028	2	Q6Z682	Q6z682 rattus norv	371	197.5	10.9	1235	2	Q86BD5	Q86bd5 drosophila
299	205.5	11.4	2016	2	Q8MKM6	Q8mk6 drosophila	372	197.5	10.9	1235	2	Q9V787	Q9v787 drosophila
300	205.5	11.4	2016	2	Q8KEM7	Q8km7 drosophila	373	197.5	10.9	1240	1	NFAS_MOUSE	Q810u3 mus musculu
301	205.5	11.4	2019	2	Q8MKM8	Q8km8 drosophila	374	197.5	10.9	1251	2	Q6ZQ54	Q6zq54 mus musculu
302	205.5	11.4	17352	2	Q95YM2	Q95ym2 procambarus	375	197.5	10.9	1447	1	DCC_HUMAN	P43146 homo sapien
303	205	11.4	432	2	Q5OJUP1	Q5ojup1 homo sapien	376	197.5	10.9	16215	2	Q9NFS3	Q9nfs3 drosophila
304	204.5	11.3	439	2	O57349	O57349 gallus gall	377	197.5	10.9	18074	2	Q917U4	Q917u4 drosophila
305	204.5	11.3	1377	1	NEO1_RAT	P97603 rattus norv	378	197	10.9	537	2	Q7PSJ8	Q7psj8 anopheles g
306	204.5	11.3	1675	2	Q98SW4	Q98sw4 brachydanio	379	196	10.9	1240	1	NFAS_HUMAN	Q94856 homo sapien
307	204.5	11.3	3197	2	Q9WID5	Q9wid5 drosophila	380	196	10.9	1906	1	KMLS_CHICK	P11799 gallus gall
308	204	11.3	430	2	Q7QGS8	Q7qgs8 anopheles g	381	195.5	10.8	1270	2	Q9U3P2	Q9u3p2 caenorhabdi
309	204	11.3	1443	1	NEO1_CHICK	Q90610 gallus gall	382	195	10.8	1369	1	NFAS_CHICK	Q42412 gallus gall
310	203.5	11.3	1249	2	Q90Z04	Q90z04 xenopus lae	383	195	10.8	1375	2	Q8ML47	Q8ml47 drosophila
311	203.5	11.3	1316	2	Q7QEI6	Q7qeie6 anopheles g	384	195	10.8	1375	2	Q94537	Q94537 drosophila
312	203.5	11.3	2053	2	Q8XU7	Q8xuu7 homo sapien	385	195	10.8	1386	1	ROB3_HUMAN	Q945m0 homo sapien
313	203.5	11.3	2092	2	Q76MU9	Q76mu9 homo sapien	386	195	10.8	1526	2	Q94538	Q94538 drosophila
314	203.5	11.3	2113	2	Q8TDB4	Q8tdb4 homo sapien	387	195	10.8	1526	2	Q9V6D5	Q9v6d5 drosophila
315	203	11.2	483	2	Q7SX76	Q7sxx76 brachydanio	388	194.5	10.8	1277	1	CAML_FUGRU	Q98902 fugu rubrip
316	203	11.2	1006	2	Q6IDE9	Q6ide9 drosophila	389	194	10.7	949	2	Q9VWZ7	Q9vwz7 drosophila
317	203	11.2	1415	2	Q94155	Q94155 caenorhabdi	390	193.5	10.7	1256	1	NFCA_MOUSE	Q810u4 mus musculu
318	203	11.2	1950	2	Q8QYN8	Q8qyn8 mus musculu	391	193	10.7	749	2	Q967D9	Q967d9 drosophila
319	202.5	11.2	496	2	Q7Z075	Q7z075 caenorhabdi	392	193	10.7	775	2	Q6PF50	Q6pf50 xenopus lae
320	202.5	11.2	1066	2	Q8MSR5	Q8msr5 drosophila	393	193	10.7	802	2	Q80ZF5	Q80zf5 rattus norv
321	202.5	11.2	1946	2	Q68J72	Q68j72 apis mellif	394	193	10.7	902	2	Q8IQ17	Q8iq17 drosophila
322	202.5	11.2	2828	2	Q9NR99	Q9nr99 homo sapien	395	193	10.7	903	2	Q967D8	Q967d8 drosophila
323	202	11.2	947	1	MUSK_CHICK	Q8axy6 gallus gall	396	193	10.7	903	2	Q9VQY1	Q9vqy1 drosophila

105	260.5	14.4	500	2	Q9W260	Q9W260 drosophila	178	229.5	12.7	869	1	MUSK_HUMAN	O15146 homo sapien
106	260.5	14.4	500	2	Q9XZB7	Q9XZB7 drosophila	179	229	12.7	1056	1	Q9OZ03	Q9OZ03 xenopus lae
107	260	14.4	601	2	Q96CJ3	Q96CJ3 homo sapien	180	229	12.7	4391	1	PGBM_HUMAN	P98160 homo sapien
108	260	14.4	1395	2	Q7KVK3	Q7KVK3 drosophila	181	228.5	12.7	1040	2	Q9W675	Q9W675 brachydanio
109	260	14.4	1429	2	Q9W213	Q9W213 drosophila	182	228.5	12.7	1117	2	Q8P1C6	Q8P1C6 mus musculus
110	259	14.3	7962	2	Q10465	Q10465 homo sapien	183	228	12.6	1028	2	Q8C6X1	Q8C6X1 mus musculus
111	259	14.3	34350	2	Q8WZ42	Q8WZ42 homo sapien	184	227.5	12.6	1051	1	PTK7_CHICK	Q91048 gallus gall
112	258.5	14.3	395	2	Q8BXJ7	Q8BXJ7 m mus muscu	185	227.5	12.6	1099	2	P97527	P97527 rattus norv
113	258.5	14.3	395	2	Q8BZP4	Q8BZP4 mus musculus	186	227	12.6	1189	2	Q9P2J2	Q9P2J2 homo sapien
114	258.5	14.3	404	2	Q8BLOQ	Q8BLOQ mus musculus	187	226.5	12.5	476	2	Q6AYP5	Q6AYP5 rattus norv
115	258.5	14.3	404	2	Q8BYP1	Q8BYP1 mus musculus	188	226	12.5	6632	1	UN89_CAEEL	Q81761 caenorhabdi
116	257	14.2	1056	2	Q7ZW34	Q7ZW34 brachydanio	189	226	12.5	8081	2	Q7Z120	Q7Z120 caenorhabdi
117	256	14.2	256	2	Q8N3J6	Q8N3J6 homo sapien	190	225.5	12.5	868	1	MUSK_MOUSE	Q61006 mus musculus
118	255.5	14.1	838	2	Q90YMI	Q90YMI brachydanio	191	225.5	12.5	1388	2	Q7QKD0	Q7QKD0 anopheles g
119	255	14.1	359	1	LACH_DROME	Q24372 drosophila	192	225.5	12.5	1662	2	Q7QIV4	Q7QIV4 anopheles g
120	255	14.1	359	2	Q9V6C2	Q9V6C2 drosophila	193	224.5	12.4	1224	2	Q00533	Q00533 homo sapien
121	254.5	14.1	5175	2	Q810L3	Q810L3 caenorhabdi	194	224	12.4	390	2	Q9H1X9	Q9H1X9 homo sapien
122	254.5	14.1	5198	2	Q7F5I8	Q7F5I8 caenorhabdi	195	224	12.4	697	2	Q8NC72	Q8NC72 homo sapien
123	251.5	13.9	837	1	NCM2_MOUSE	Q35136 mus musculus	196	224	12.4	1059	2	Q6UXL7	Q6UXL7 homo sapien
124	250.5	13.9	1342	2	Q9GPP6	Q9GPP6 drosophila	197	224	12.4	1119	2	Q6UXM1	Q6UXM1 homo sapien
125	250.5	13.9	1342	2	Q9VPZ7	Q9VPZ7 drosophila	198	224	12.4	1252	2	Q96DN3	Q96DN3 homo sapien
126	250	13.8	349	1	LACH_SCHAM	Q26474 schistocerc	199	223	12.3	417	2	Q7TNL1	Q7TNL1 mus musculus
127	250	13.8	525	2	Q7FZS8	Q7FZS8 anopheles g	200	222	12.3	450	2	Q9VR25	Q9VR25 drosophila
128	250	13.8	795	2	Q90YMO	Q90YMO brachydanio	201	222	12.3	595	2	Q6ZRS5	Q6ZRS5 homo sapien
129	250	13.8	955	1	MDG1_HUMAN	Q8NFP4 homo sapien	202	221.5	12.3	862	1	CD22_MOUSE	P35329 mus musculus
130	249.5	13.8	1040	1	AXO1_HUMAN	Q02246 homo sapien	203	221	12.2	435	2	Q8WR44	Q8WR44 caenorhabdi
131	246.5	13.6	627	2	Q8N466	Q8N466 homo sapien	204	221	12.2	436	2	Q8MPV1	Q8MPV1 caenorhabdi
132	246.5	13.6	727	2	Q6RKB2	Q6RKB2 rattus norv	205	221	12.2	1340	2	Q8NDA2	Q8NDA2 homo sapien
133	246.5	13.6	837	2	Q6RKB3	Q6RKB3 rattus norv	206	221	12.2	1746	2	Q8WY19	Q8WY19 homo sapien
134	246.5	13.6	865	2	Q68DA2	Q68DA2 homo sapien	207	221	12.2	1827	2	Q9VSG5	Q9VSG5 drosophila
135	246.5	13.6	1018	1	CONT_HUMAN	Q12860 homo sapien	208	221	12.2	2012	1	DSCA_HUMAN	O60469 homo sapien
136	245.5	13.6	1065	1	LIG2_HUMAN	Q94898 homo sapien	209	220.5	12.2	333	2	Q86WB8	Q86WB8 homo sapien
137	245	13.6	1028	2	Q6INB5	Q6INB5 xenopus lae	210	220.5	12.2	336	2	Q8OVG4	Q8OVG4 mus musculus
138	244.5	13.5	512	2	Q96DN8	Q96DN8 homo sapien	211	220.5	12.2	336	2	Q9D6E7	Q9D6E7 mus musculus
139	243.5	13.5	837	2	Q7Z7F2	Q7Z7F2 homo sapien	212	220.5	12.2	428	2	Q6F3J3	Q6F3J3 mus musculus
140	243.5	13.5	949	1	MDC1_MOUSE	P60755 mus musculus	213	220.5	12.2	443	2	Q8N2F4	Q8N2F4 homo sapien
141	243.5	13.5	956	1	MDC1_HUMAN	Q72553 homo sapien	214	220.5	12.2	445	2	Q8K3T6	Q8K3T6 mus musculus
142	243.5	13.5	1021	1	CONT_RAT	P12960 mus musculus	215	220.5	12.2	445	2	Q8R4L1	Q8R4L1 mus musculus
143	243.5	13.5	1036	1	AXO1_CHICK	P28685 gallus gall	216	220.5	12.2	456	2	Q8R5M8	Q8R5M8 mus musculus
144	242.5	13.4	949	1	MDC1_RAT	P60756 rattus norv	217	220.5	12.2	898	1	FAS2_SCHAM	P22648 schistocerc
145	242.5	13.4	1020	2	Q6NXXV7	Q6NXXV7 mus musculus	218	220	12.2	1043	2	Q6PA07	Q6PA07 xenopus lae
146	241.5	13.4	837	1	NCM2_HUMAN	O15394 homo sapien	219	220	12.2	1614	2	Q8UVD7	Q8UVD7 xenopus lae
147	241.5	13.4	1018	2	Q28106	Q28106 bos taurus	220	219.5	12.2	330	2	Q90Z42	Q90Z42 gallus gall
148	241.5	13.4	1020	1	CONT_MOUSE	P12960 mus musculus	221	219.5	12.2	390	2	Q66KX2	Q66KX2 xenopus lae
149	240.5	13.3	757	2	Q7OCU0	Q7OCU0 anopheles g	222	219.5	12.2	442	2	Q9BY67	Q9BY67 homo sapien
150	240	13.3	3707	1	PGBM_MOUSE	Q05793 mus musculus	223	219	12.1	1009	2	Q93250	Q93250 xenopus lae
151	237.5	13.2	702	2	Q6S2Y8	Q6S2Y8 mus musculus	224	219	12.1	1026	2	Q81WV2	Q81WV2 homo sapien
152	237	13.1	312	2	Q66KV0	Q66KV0 xenopus lae	225	219	12.1	1062	2	Q8BK93	Q8BK93 mus musculus
153	235.5	13.0	632	2	Q62RK5	Q62RK5 homo sapien	226	219	12.1	1091	1	LIG1_MOUSE	P70193 mus musculus
154	235.5	13.0	1027	2	Q90W79	Q90W79 gallus gall	227	219	12.1	1093	1	LIG1_HUMAN	Q96JAI homo sapien
155	235.5	13.0	2623	2	Q6WR10	Q6WR10 homo sapien	228	219	12.1	4071	2	Q6KDZ1	Q6KDZ1 gallus gall
156	234.5	13.0	358	2	Q90490	Q90490 brachydanio	229	218.5	12.1	1114	2	Q9BWV1	Q9BWV1 homo sapien
157	234.5	13.0	779	2	Q97136	Q97136 manduca sex	230	218.5	12.1	1115	2	Q8UXJ5	Q8UXJ5 homo sapien
158	234.5	13.0	837	2	Q97137	Q97137 manduca sex	231	218.5	12.1	1612	1	ROB1_MOUSE	Q80266 mus musculus
159	234.5	13.0	1040	1	AXO1_RAT	P22063 rattus norv	232	218	12.1	705	2	Q8CB03	Q8CB03 mus musculus
160	233.5	12.9	1026	2	Q94780	Q94780 homo sapien	233	218	12.1	2013	2	Q9VHZ8	Q9VHZ8 rattus norv
161	233.5	12.9	1100	2	Q94779	Q94779 homo sapien	234	218	12.1	2013	2	Q9ERC8	Q9ERC8 mus musculus
162	233	12.9	394	2	Q7ZXX1	Q7ZXX1 xenopus lae	235	217.5	12.0	348	2	Q00557	Q00557 homo sapien
163	233	12.9	1028	2	P97528	P97528 rattus norv	236	217.5	12.0	1555	2	Q7PPH8	Q7PPH8 anopheles g
164	232.5	12.9	2793	2	Q8ISF3	Q8ISF3 caenorhabdi	237	217	12.0	885	2	Q8HYV1	Q8HYV1 sus scrofa
165	232.5	12.9	2608	2	Q8ISF4	Q8ISF4 caenorhabdi	238	217	12.0	886	2	Q8HYV2	Q8HYV2 sus scrofa
166	232.5	12.9	18519	2	Q8ISF6	Q8ISF6 caenorhabdi	239	217	12.0	1443	2	Q9MTB2	Q9MTB2 drosophila
167	232.5	12.9	18534	2	Q8ISF7	Q8ISF7 caenorhabdi	240	217	12.0	1765	2	Q9VS30	Q9VS30 drosophila
168	231.5	12.8	858	2	O18466	O18466 hirudo medi	241	217	12.0	1770	2	Q9VS29	Q9VS29 drosophila
169	231.5	12.8	1005	2	P79921	P79921 xenopus lae	242	216.5	12.0	1109	2	Q6P5H3	Q6P5H3 mus musculus
170	231	12.8	703	2	Q21139	Q21139 caenorhabdi	243	215.5	11.9	286	2	Q7PF93	Q7PF93 anopheles g
171	231	12.8	1028	2	Q9UQ52	Q9UQ52 homo sapien	244	215.5	11.9	497	2	Q9BXN7	Q9BXN7 homo sapien
172	231	12.8	1028	2	Q9JMB8	Q9JMB8 mus musculus	245	215.5	11.9	714	2	Q6ZPE6	Q6ZPE6 mus musculus
173	230.5	12.8	807	2	Q6NY23	Q6NY23 brachydanio	246	215.5	11.9	886	2	Q9VM64	Q9VM64 drosophila
174	230.5	12.8	868	1	MUSK_RAT	Q62838 rattus norv	247	215.5	11.9	1302	1	NRG_DROME	P20241 drosophila
175	230.5	12.8	1032	2	Q8UVD6	Q8UVD6 brachydanio	248	215.5	11.9	2597	2	Q8WRH9	Q8WRH9 rattus norv
176	230.5	12.8	1040	1	AXO1_MOUSE	Q61330 mus musculus	249	215	11.9	443	2	Q8WR43	Q8WR43 caenorhabdi
177	229.5	12.7	510	2	Q801V8	Q801V8 brachydanio	250	215	11.9	444	2	Q8MPU9	Q8MPU9 caenorhabdi

OM protein - protein search, using sw model

Run on: June 3, 2005, 14:25:22 ; Search time 175 Seconds
(without alignments)
1006.601 Million cell updates/sec

Title: US-09-978-544A-523
Perfect score: 1806
Sequence: 1 MKTIQPMHNSWIAIFTL.....RRAGCVLLPLLVHLLKX 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1780	98.6	344	2	QB8G33 m mus muscu
2	1665.5	92.2	344	1	NTRI_HUMAN
3	1647.5	91.2	344	1	NTRI_MOUSE
4	1639.5	90.8	344	1	NTRI_RAT
5	1477.5	81.8	353	1	CEPU_CHICK
6	1428	79.1	313	2	O57596
7	1427.5	79.0	344	2	O93242
8	1357.5	75.2	315	2	O9DGL5
9	1306	72.3	337	2	Q8DFY2
10	1305	72.3	337	1	OPCM_CHICK
11	1295.5	71.7	338	2	Q723W6
12	1276.5	70.7	345	2	Q6GM08
13	1275.5	70.6	344	2	Q9DF61
14	1270.5	70.3	344	2	Q6B014
15	1268	70.2	345	1	OPCM_HUMAN
16	1266	70.1	345	1	OPCM_BOVIN
17	1259	69.7	345	1	OPCM_RAT
18	993.5	55.0	342	2	Q64280
19	946	52.4	334	2	O02870
20	938.5	52.0	338	1	LAMP_CHICK
21	931.5	51.6	338	1	LAMP_HUMAN
22	930.5	51.5	350	2	O02869
23	926.5	51.3	337	1	LAMP_RAT
24	904	50.1	337	2	Q6GL27
25	894	49.5	341	1	LAMP_MOUSE
26	842	46.6	352	2	Q9W6V2
27	823	45.6	352	1	NEGR_HUMAN
28	815	45.1	348	1	NEGR_RAT
29	814	45.1	348	1	NEGR_MOUSE
30	759	42.0	325	2	QBHW98
31	686.5	38.0	188	2	QB8MT5 m mus muscu

Q80T70 mus musculu	2	Q80T70	262	36.4	656.5	32
Q9W6V1 gallu	2	Q9W6V1	261	33.2	599	33
Q8N440 homo sapien	2	Q8N440	226	30.2	545.5	34
Q9VMN6 drosophila	2	Q9VMN6	606	21.1	380.5	35
Q7Q154 anopheles g	2	Q7Q154	303	20.3	367	36
Q7Q863 anopheles g	2	Q7Q863	320	19.9	359.5	37
Q7Q0P8 anopheles g	2	Q7Q0P8	320	19.8	358	38
Q8IP70 drosophila	2	Q8IP70	672	19.4	350.5	39
Q6NNU3 drosophila	2	Q6NNU3	532	19.4	349.5	40
Q9VLF0 drosophila	2	Q9VLF0	532	19.4	349.5	41
Q9W4R3 drosophila	2	Q9W4R3	554	19.3	348	42
Q7Q864 anopheles g	2	Q7Q864	301	19.2	346	43
Q7Q0P9 anopheles g	2	Q7Q0P9	316	18.9	341	44
Q9VAR6 drosophila	2	Q9VAR6	413	18.7	338	45
Q7Q8F3 anopheles g	2	Q7Q8F3	299	18.7	338	46
Q9VMB2 drosophila	2	Q9VMB2	315	18.4	333	47
Q7QCH7 anopheles g	2	Q7QCH7	399	18.2	328	48
Q7Q807 anopheles g	2	Q7Q807	340	17.6	318	49
Q9VMN9 drosophila	2	Q9VMN9	550	17.3	313	50
Q7PN14 anopheles g	2	Q7PN14	285	17.3	312.5	51
P91670 drosophila	2	P91670	528	17.1	308.5	52
Q9VCT4 drosophila	2	Q9VCT4	545	16.9	306	53
Q7QBV2 anopheles g	2	Q7QBV2	413	16.9	305	54
Q8WPB3 drosophila	2	Q8WPB3	316	16.8	303.5	55
Q8WP94 drosophila	2	Q8WP94	316	16.6	300.5	56
Q9VME2 drosophila	2	Q9VME2	948	16.6	300	57
Q7PSS8 anopheles g	2	Q7PSS8	401	16.6	299	58
Q8WP58 drosophila	2	Q8WP58	316	16.5	297.5	59
P15364 drosophila	2	P15364	333	16.5	297.5	60
Q7KX2 drosophila	1	AMAL_DROME	333	16.5	297.5	61
Q7QBC5 anopheles g	2	Q7QBC5	341	16.5	297.5	62
Q7PXA4 anopheles g	2	Q7PXA4	383	16.3	294.5	63
Q96SC3 homo sapien	2	Q96SC3	2673	16.1	280.5	64
Q96RW7 homo sapien	2	Q96RW7	5636	16.1	280.5	65
Q57577 cynops pyrr	2	Q57577	846	15.9	287	66
Q57576 cynops pyrr	2	Q57576	1100	15.9	287	67
Q7QBV1 anopheles g	2	Q7QBV1	413	15.8	285.5	68
Q9NKF5 drosophila	2	Q9NKF5	603	15.8	285.5	69
Q9VP08 drosophila	2	Q9VP08	403	15.7	284	70
P13594 mus musculu	2	NCA2_MOUSE	725	15.7	283.5	71
P13595 mus musculu	2	NCA1_MOUSE	1115	15.7	283.5	72
Q921P2 mus musculu	2	Q921P2	605	15.6	282.5	73
Q8BQ96 mus musculu	2	Q8BQ96	838	15.6	282.5	74
Q8C4B2 mus musculu	2	Q8C4B2	838	15.6	282.5	75
Q73633 xenopus lae	2	Q73633	725	15.5	279.5	76
P13590 gallus gall	2	NCA1_CHICK	1091	15.5	279.5	77
Q98918 gallus gall	1	Q98918	4162	15.4	278.5	78
Q661V0 xenopus lae	2	Q661V0	719	15.4	277.5	79
P13596 rattus norv	2	NCA1_RAT	858	15.4	277.5	80
P16170 xenopus lae	1	NCA1_XENLA	1088	15.4	277.5	81
Q6PFK4 brachydanio	2	Q6PFK4	405	15.3	276.5	82
P13592 homo sapien	2	NCA2_HUMAN	761	15.3	276	83
P13591 homo sapien	2	NCA1_HUMAN	848	15.3	276	84
P31836 bos taurus	2	NCA1_BOVIN	853	15.3	275.5	85
Q73634 xenopus tro	2	Q73634	725	15.1	273.5	86
Q6DJ83 xenopus tro	2	Q6DJ83	433	15.1	272.5	87
Q8476 gallus gall	2	Q8476	1323	15.1	272.5	88
Q86X47 homo sapien	2	Q86X47	858	15.0	271	89
P36335 xenopus lae	2	NCA2_XENLA	1092	15.0	270.5	90
Q7QKT5 drosophila	2	Q7QKT5	1479	15.0	270	91
Q26475 schistocerc	2	Q26475	484	14.9	269.5	92
Q92626 homo sapien	2	Q92626	1496	14.9	268.5	93
Q7P8N2 anopheles g	2	Q7P8N2	392	14.7	265	94
Q9V4Y0 drosophila	2	Q9V4Y0	1482	14.7	265	95
Q7PRK4 anopheles g	2	Q7PRK4	1185	14.6	264.5	96
Q7QBA7 anopheles g	2	Q7QBA7	316	14.6	263	97
Q80U60 mus musculu	2	Q80U60	1431	14.6	263	98
Q80U60 mus musculu	2	Q80U60	1431	14.6	263	99
Q7YRFS canis famil	2	Q7YRFS	3950	14.5	261.5	100
Q8IZP8 homo sapien	2	Q8IZP8	437	14.5	261.5	101
P14781 gallus gall	2	CONT_CHICK	1010	14.5	261	102
Q90Y2M brachydanio	1	Q90Y2M	1031	14.5	261	103
O44924 drosophila	2	O44924	1395	14.5	261	104
Q7TN00 rattus norv	2	Q7TN00	3410	14.5	261	104

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R;Small, S.J.; Akeson, R.
J. Cell Biol. 111, 2089-2096, 1990
A;Title: Expression of the unique NCAM VASE exon is independently regulated in distinct
A;Reference number: A37795; MUID:91035620; PMID:1699951
A;Accession: B37795
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 340-381 <SM2>
R;Small, S.J.; Haines, S.L.; Akeson, R.A.
Neuron 1, 1007-1017, 1988
A;Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev
A;Reference number: F58136; MUID:90166485; PMID:2483093
A;Accession: F58136
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 353-364 <RES>
A;Cross-references: GB:M32611; NID:G205643; PIDN:AAA41679.1; PID:G205644
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Various forms of NCAM are produced by alternative splicing.
C;Genetics:
A;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-858/Product: neural cell adhesion molecule, short domain form #status predicted <MA
F;20-721/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMW3>
F;263-272/Region: NCAM binding #status predicted
F;323-398/Domain: immunoglobulin homology <IMW4>
F;430-492/Domain: immunoglobulin homology <IMW5>
F;529-606/Domain: fibronectin type III repeat homology <FN3A>
F;635-695/Domain: fibronectin type III repeat homology <FN3B>
F;727-739/Domain: transmembrane #status predicted <TM>
F;740-858/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-288,330-396,437-490/Disulfide bonds: #status predicted
F;222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.4%; Score 277.5; DB 1; Length 858;
Best Local Similarity 25.5%; Pred. No. 1.5e-12;
Matches 75; Conservative 50; Mismatches 132; Indels 37; Gaps 7;
Qy 44 NTVRQGESATLRCTIDN-RVTRVAVLNRSTILYAGNDKWLCDPRVLLSNTQYYSIEI 102
Db 222 NATANLGOSVTLVCDADGFPPTMSWTGKGPIENEER---DDEKHIFSDSSE--LTI 275
Qy 103 QNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGR 162
Db 276 RNVKNDDEAYVCIAENKAGEQDASIHLLKVPAPKITYVENQTAMELEBEQVTLTCEASGD 335
Qy 163 PEPTVTWR-----HISKAVGFVSEDEYLEIQGITREQSG 197
Db 336 PIPSITWRTSTRNISSEBKASWTRPEKQETLDGHWVYSHARVSS---LTLKSTQYTDAG 392
Qy 198 DYECASNDVAAPVVRVKVTVPYPISEAKGTGVPVVGQKGTLOCEASAVPSAEFQYK 257
Db 393 EYICATSNITGQD--SQSMYLEVQVAPKLGQPVAVTVWEGNVNITCEVFAYPSATISGWFR 451
Qy 258 DDKELIEGK-KGVKVENRPFLSKLFFNVSEHDYGNVTCVASNKLGHNTNASIML 310
Db 452 DGQLLPSNYSNIKIYTPSASYLEVTVPDSENDFGNVNTAVNRIGQESLEFIL 505

RESULT 15

LUXLNL
neural cell adhesion molecule long domain form precursor - African clawed frog
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004

C;Accession: S09600
R;Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res 17, 10321-10335, 1989
A;Title: Primary structure and developmental expression of a large cytoplasmic domain fo
A;Reference number: S09600; MUID:90098871; PMID:2481269
A;Accession: S09600
A;Molecule type: mRNA
A;Residues: 1-1088 <KRI>
A;Cross-references: UNIPROT:P16170; EMBL:M25696; NID:G214609; PIDN:AAA49909.1; PID:G2146
A;Note: the authors translated the codon AAA for residue 970 as Leu
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Several forms of NCAM are produced by alternative splicing.
C;Genetics:
A;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <LD
F;20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status pre
F;20-705/Domain: extracellular #status predicted <EXT>
F;34-95/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;225-284/Domain: immunoglobulin homology <IMM3>
F;317-381/Domain: immunoglobulin homology <IMM4>
F;413-475/Domain: immunoglobulin homology <IMM5>
F;512-589/Domain: fibronectin type III repeat homology <FN3A>
F;618-679/Domain: fibronectin type III repeat homology <FN3B>
F;706-723/Domain: transmembrane #status predicted <TM>
F;724-1088/Domain: intracellular #status predicted <INT>
F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F;219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.4%; Score 277.5; DB 1; Length 1088;
Best Local Similarity 27.9%; Pred. No. 2.1e-12;
Matches 80; Conservative 49; Mismatches 121; Indels 37; Gaps 11;
Qy 44 NTVRQGESATLRCTIDN-RVTRVAVLNRSTILYAGNDKWLCDPRVLLSNTQYYSIEI 102
Db 219 NATANMAESVVLSCDADGFPDPEISWLKGEPIEDGEK-----ISFNQSEMTI 269
Qy 103 QNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGR 162
Db 270 HHVEKDEAEVSCYANNQAGEAEATILLKVYAKPKITYVENKTAV-ELDEITLTCEASGD 328
Qy 163 PEPTVTW---RHISPKAV---GFVSEDEYLEIQGITRE-----QSGDYECASNDVAAP 210
Db 329 PIPSITWRTAVRNISSEATLDGHIIVVKEHIRMALTLKDIQYTDAGEYFCIASNPICGVD 388
Qy 211 VVRVKVTVPYPISEAKGTGVPV-----GQKGTLOCEASAVPSAEFQYKDKRLIE 264
Db 389 -MQAMYFEVQYAPKI---RG---EVVYTVWEGNVNITCEVFAPRAAVTVFRDQQLLPS 441
Qy 265 GK-KGVKVENRPFLSKLFFNVSEHDYGNVTCVASNKLGHNTNASIML 310
Db 442 SNFSNIIKISGPTSSSLEVPDSENDFGNVNTAVNRIGHEFSEFIL 488

Search completed: June 3, 2005, 14:38:54

Job time : 51 secs

A1923
amalgam protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 09-Jul-2004
C:Accession: A31923
R:Seeger, M.A.; Haffley, L.; Kaufman, T.C.
Cell 55, 589-600, 1988
A:Title: Characterization of amalgam: a member of the immunoglobulin superfamily from D.
A:Reference number: A31923; MUID:89028670; PMID:3141062
A:Accession: A31923
A:Molecule type: DNA
A:Residues: 1-333 <SE>
A:Cross-references: UNIPROT: P15364; GB: M23561; NID: g156920; PID: AAA28367.1; PID: g156921
C:Genetics:
A:Gene: FlyBase: Ama
A:Cross-references: FlyBase: FBgn0000071

Query Match 16.5%; Score 297.5; DB 2; Length 333;
Best Local Similarity 29.7%; Pred. No. 1.5e-14;
Matches 87; Conservative 43; Mismatches 136; Indels 27; Gaps 11;

QY 44 NVTVRQGESATURCTIDN-RVTRVAWLNR-----STLYAGNDKWCCLDPR--VVLLSN 93
DB 33 DVVASGVDSVFNCTVEEVQGLSVSWAKRPESDTSNVLSMRNLSLPDKRYNVTVEG 92

QY 94 TOTQ---YSIEIQNVVDYDEGPTCSVQTDNHPK-TSRVHLIVQSPKIVE-ISSDISIN 148
DB 93 PKTGSATYFTRIONIEVSDMGPEYECQVLVSATEKVTKLSLQIKTPPVIAENTPKSTLVT 152

QY 149 EGNINSLTICATGRPEPTVTRH-----ISPKAVGVFSEDEYLEIOGITREQSGDYECAS 204
DB 153 EGNLELTCHANGFPKPTTSWAREHNVMP-AGGHLLAEPTLIRSVHRMDRGGYCIAQ 211

QY 205 NDVAAPVVRVRVTVNYPYIS-EAKGTGVPVQKGTQCEASAVPSAEFQWKDKKLI 263
DB 212 NEEGQPKRLIRVEFRQIAVQPKTAQMVSAAELSCSVQGPAPTVVWKKGVPL- 270

QY 264 EGKGVKVENR-----PFLSKLIFNVSEHDYGNVTCVASNKLGHNTASIMLF 311
DB 271 QSSRHHEVANTASSSTTTSLRIDSVBGEEDFGDYCNATNKLGHADARLHLF 323

RESULT 9
IUMSNG
neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse
N:Alternate names: NCAM-120
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
R:Barthele, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec
EMBO J. 6, 907-914, 1987
A:Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A:Reference number: A29673; MUID:87246524; PMID:3595563
A:Accession: A29673
A:Molecule type: mRNA
A:Residues: 1-725 <BA>
A:Cross-references: UNIPROT: P13594; EMBL: Y00051; NID: g53342; PIDN: CAA68263.1; PID: g53343
R:Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A:Title: Differential splicing and alternative polyadenylation generates distinct NCAM
A:Reference number: S00382; MUID:88283628; PMID:3396534
A:Accession: S00382
A:Molecule type: DNA
A:Residues: 642-656, 'D', 658-725 <BA2>
A:Cross-references: EMBL: X07195
R:Aougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A:Title: Structural and immunological characterization of the amino-terminal domain of
A:Reference number: A44290; MUID:86140120; PMID:3512556
A:Accession: A44290
A:Molecule type: protein
A:Residues: 20-36 <RO>
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol

C:Comment: Several forms of NCAM are produced by alternative splicing. See also PIR: IUMS
C:Genetics:
A:Gene: NCAM
A:Map position: 9
A:Introns: 701/1
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C:Keywords: alternative splicing; cell adhesion; signal sequence #status predicted <SIG>
F:1-19/Domain: signal sequence #status predicted <SIG>
F:34-98/Domain: immunoglobulin homology <IMM1>
F:132-191/Domain: immunoglobulin homology <IMM2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:228-290/Domain: immunoglobulin homology <IMM3>
F:263-272/Region: NCAM binding #status predicted
F:323-388/Domain: immunoglobulin homology <IMM4>
F:420-482/Domain: immunoglobulin homology <IMM5>
F:519-596/Domain: fibronectin type III repeat homology <FN3A>
F:623-685/Domain: fibronectin type III repeat homology <FN3B>
F:41-96, 139-189, 235-288, 330-386, 427-480/Disulfide bonds: #status predicted
F:222, 316, 348, 424, 450, 479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.7%; Score 283.5; DB 1; Length 725;
Best Local Similarity 25.8%; Pred. No. 4.4e-13;
Matches 75; Conservative 45; Mismatches 130; Indels 41; Gaps 7;

QY 44 NVTVRQGESATURCTIDN-RVTRVAWLNRSTLYAGNDKWCCLDPRVV-----LLSNTQ 95
DB 222 NATANLGQSVTLVCDADG-----FPEPTM-----SWTKDGEPIENEEDERSRSVS 268

QY 96 TOYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQSPKIVEISSDISINEGNISL 155
DB 269 DSSEVTIRNVDDKAEAYVCIENKAGQDASIIHLKVPKPKITVYENQTAMELEEQVTL 328

QY 156 TCIATGRPEPTVTR-----HISPKAVGVFSEDEYLEIOGITREQSGDYE 200
DB 329 TCEASGDPIPSITWKTSTRNISSEBQDLGDGHVVRSHARVS---LTKLSQYRDAGEYM 385

QY 201 CSASNDAAVVRVRVTVNYPYISEAKGTGVPVQKGTQCEASAVPSAEFQWKDK 260
DB 386 CTASNTIQD--SQSIDLEFQYAPKLGQPVAVTVWEGNVNITCEVAFVPSATISWFRDQ 444

QY 261 RLIEGK-KGVKVENRPPFLSKLIFNVSEHDYGNVTCVASNKLGHNTASIML 310
DB 445 LLPSSNYSNIKITYNTPSASYLEVTPDSEDFGNYNCTAVNRIGQESLEFIL 495

RESULT 10
IUMSML
neural cell adhesion molecule 1 precursor, long domain splice form - mouse
N:Alternate names: NCAM-180
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
R:Barthele, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec
EMBO J. 6, 907-914, 1987
A:Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A:Reference number: A29673; MUID:87246524; PMID:3595563
A:Accession: A29673
A:Molecule type: mRNA
A:Residues: 1-548, 'T', 550-571, 'T', 573-574, 'D', 576-588, 'MQPS', 593, 'S', 595-599, 'P', 601, 'L',
A:Cross-references: UNIPROT: P13595; EMBL: Y00051; NID: g53342; PIDN: CAA68263.1; PID: g53343
R:Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.;
Nucleic Acids Res. 15, 8621-8641, 1987
A:Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse neu
A:Reference number: S00844; MUID:88067687; PMID:3684567
A:Accession: S00844
A:Molecule type: mRNA
A:Residues: 523-809, 1077-1115 <SAN>
A:Cross-references: EMBL: X06328; NID: g53322; PIDN: CAA29641.1; PID: g817984
R:Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A:Title: Differential splicing and alternative polyadenylation generates distinct NCAM

A:Molecule type: mRNA
A:Residues: 1-338 <LIP>
A:Cross-references: UNIPROT:P2736; GB:M88709; NID:G203245; PIDN:AAA0858.1; PID:G203246
A:Experimental source: brain
C:Genetics:
A:Gene: OBCAM
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 71.2%; Score 1285.5; DB 2; Length 338;
Best Local Similarity 71.6%; Pred. No. 2.8e-87;
Matches 242; Conservative 35; Mismatches 60; Indels 1; Gaps 1;

QY 8 MNSISWALFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLCTIDNRVTRVA 67
DB 1 MYHPAYWIVSATALLFPGVPRSGDATFPKAMDNVTVRQGESATLCTIDNRVTRVA 60
QY 68 WLNRSITLYAGNDKWLDRVLLSNTQYISIEIONVDYDEGPTVCSVQTDNHPKTSR 127
DB 61 WLNRSITLYAGNDKWSIDPRVILVNTPTQYSIMIQNVVDYDEGPTVCSVQTDNHPKTSR 120
QY 128 VHLIVQSPKIVEISSDISINEGNISLTCTATGRPEPTVTVRHHISPK-AVGFSVEDEYL 186
DB 121 VHLIVQSPQIMNISSDITVNEISSVTLLCLAIGRPEPTVTVRHHLSVKEGQGFVSEDEYL 180
QY 187 EQGITREOSGDYECASNDVAAPVVRVKVTYVPPYIIEAKGTGVPVQKGTLOCEAS 246
DB 181 EISDIKRDQSGEYCSALNDVAAPVVRVKVTYVPPYIIEAKGTGVPVQKGTLOCEAS 240
QY 247 AVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTNA 306
DB 241 AVPMAEFQWKEDTRLATGLDGMRIENKGRMSTLTFFNVSEKDYGNVTCVATNKLGNNTNA 300
QY 307 SITMLPGGAVSEVSGNTSRRAGCVLLPLLVHLLKLF 344
DB 301 SITLPGGAVIDGVNSASRALACLMLSGTFFAHFFIKF 338

RESULT 3
JC4025
opioid-binding cell adhesion protein - human
C:Species: Homo sapiens (man)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
C:Accession: JC4025
Gene 155, 213-317, 1995
R:Shark, K.B.; Lee, N.M.
A:Title: Cloning, sequencing and localization to chromosome 11 of a cDNA encoding a huma
A:Reference number: JC4025; MUID:95237612; PMID:7721093
A:Molecule type: mRNA
A:Residues: 1-345 <SHA>
A:Cross-references: UNIPROT:Q14982; GB:L34774; NID:G514373; PIDN:AAA36387.1; PID:G514374
A:Experimental source: brain
A:Map position: 11pter-11qter
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 70.2%; Score 1268; DB 2; Length 345;
Best Local Similarity 71.2%; Pred. No. 5.7e-86;
Matches 240; Conservative 37; Mismatches 56; Indels 4; Gaps 2;

QY 12 ISWALFTGLAALCLF---QGVPRSGDATFPKAMDNVTVRQGESATLCTIDNRVTRVA 68
DB 9 LPWKCLVIVLSRLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLCTIDNRVTRVA 68
QY 69 LNRSTILYAGNDKWLDRVLLSNTQYISIEIONVDYDEGPTVCSVQTDNHPKTSRV 128
DB 69 LNRSTILYAGNDKWSIDPRVILVNTPTQYSIMIQNVVDYDEGPTVCSVQTDNHPKTSRV 128
QY 129 HLIVQSPKIVEISSDISINEGNISLTCTATGRPEPTVTVRHHISPK-AVGFSVEDEYL 187

DB 129 HLIVQSPQIMNISSDITVNEGSSVTLLCLAIGRPEPTVTVRHHLSVKEGQGFVSEDEYLE 188
QY 188 IQGITREOSGDYECASNDVAAPVVRVKVTYVPPYIIEAKGTGVPVQKGTLOCEASA 247
DB 189 ISDIKRDQSGEYCSALNDVAAPVVRVKVTYVPPYIIEAKGTGVPVQKGTLOCEASA 248
QY 248 VPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTNA 307
DB 249 VPMAEFQWKEDTRLATGLDGMRIENKGRMSTLTFFNVSEKDYGNVTCVATNKLGNNTNA 308
QY 308 IMLPGGAVSEVSGNTSRRAGCVLLPLLVHLLKLF 344
DB 309 ITLYPGGAVIDGVNSASRALACLMLSGTLLAHFFIKF 345

RESULT 4
S03199
opioid-binding protein OPCAM precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S03199
R:Schofield, P.R.; McFarland, K.C.; Hayflick, J.S.; Wilcox, J.N.; Cho, T.M.; Roy, S.; Le
EMBO J. 8, 489-495, 1989
A:Title: Molecular characterization of a new immunoglobulin superfamily protein with por
A:Reference number: S03199; MUID:89251576; PMID:2721489
A:Accession: S03199
A:Molecule type: mRNA
A:Residues: 1-345 <SCH>
A:Cross-references: UNIPROT:P11834; EMBL:X12672; NID:G585; PIDN:CAA31192.1; PID:G586
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C:Keywords: transmembrane protein
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-345/Product: opioid-binding protein OPCAM #status predicted <MAT>

Query Match 70.1%; Score 1266; DB 2; Length 345;
Best Local Similarity 71.6%; Pred. No. 8e-86;
Matches 240; Conservative 34; Mismatches 57; Indels 4; Gaps 2;

QY 14 WAIPTGLAALCLF---QGVPRSGDATFPKAMDNVTVRQGESATLCTIDNRVTRVAWL 70
DB 11 WKCLVIVLSRLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLCTIDNRVTRVAWL 70
QY 71 RSTILYAGNDKWLDRVLLSNTQYISIEIONVDYDEGPTVCSVQTDNHPKTSRVHL 130
DB 71 RSTILYAGNDKWSIDPRVILVNTPTQYSIMIQNVVDYDEGPTVCSVQTDNHPKTSRVHL 130
QY 131 IVQSPKIVEISSDISINEGNISLTCTATGRPEPTVTVRHHISPK-AVGFSVEDEYLEIQ 189
DB 131 IVQVPPQIMNISSDVTNEGSSVTLLCLAIGRPEPTVTVRHHLSVKEGQGFVSEDEYLEIS 190
QY 190 GITREOSGDYECASNDVAAPVVRVKVTYVPPYIIEAKGTGVPVQKGTLOCEASAVP 249
DB 191 DIKRDQSGEYCSALNDVAAPVVRVKVTYVPPYIIEAKGTGVPVQKGTLOCEASAVP 250
QY 250 SAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTNASIM 309
DB 251 MAEFQWKEDTRLATGLDGMRIENKGHISTLTFFNVSEKDYGNVTCVATNKLGINASIT 310
QY 310 LFGPGAVSEVSGNTSRRAGCVLLPLLVHLLKLF 344
DB 311 LYGPAGVIDGVNSASRALACLMLSGTLLFAHFFIKF 345

RESULT 5
JC1239
opioid-binding protein (clones SG8 and SG13) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: JC1239
R:Lippman, D.A.; Lee, N.M.; Loh, H.H.
Gene 117, 249-254, 1992
A:Title: Opioid-binding cell adhesion molecule (OBCAM)-related clones from a rat brain
A:Reference number: JC1238; MUID:92347701; PMID:1339369

1417 71.5 4.0 1540 2 H87203 polyketide synthas
1418 71.5 4.0 1592 2 S63208 hypothetical prote
1419 71.5 4.0 1603 1 VUKW5 vitellogenin vit-5
1420 71.5 4.0 1797 2 F69195 cell surface glyco
1421 71.5 4.0 2013 2 A11489 probable peptidogl
1422 71.5 4.0 2014 2 I36936 complement recepto
1423 71.5 4.0 2767 1 UIHU thyroglobulin prec
1424 71.5 4.0 3670 2 T36249 CDA peptide synthe
1425 71.5 4.0 4342 2 H83343 probable non-ribos
1426 71.5 4.0 5105 2 T32650 hypothetical prote
1427 71.5 4.0 6359 2 T31679 bacitracin synthe
1428 71.5 4.0 15281 2 S41309 cyclosporin synthe
1429 71 3.9 115 1 K3HUC1 Ig kappa chain pre
1430 71 3.9 115 2 T27552 T-cell receptor be
1431 71 3.9 128 2 T12517 hypothetical prote
1432 71 3.9 128 2 S40373 Ig kappa chain - h
1433 71 3.9 128 2 A56701 Ig kappa chain v r
1434 71 3.9 128 2 A26406 Ig kappa chain v r
1435 71 3.9 131 2 B32513 Ig kappa chain pre
1436 71 3.9 133 2 E82603 hypothetical prote
1437 71 3.9 139 2 G32536 T-cell receptor al
1438 71 3.9 148 2 F80116 Ig heavy chain pre
1439 71 3.9 197 2 T16627 hypothetical prote
1440 71 3.9 223 2 T09536 cytotoxic T-lympho
1441 71 3.9 224 2 F98215 transcription regu
1442 71 3.9 240 2 S06084 Ig kappa chain pre
1443 71 3.9 255 2 G83543 conserved hypotet
1444 71 3.9 261 2 AC0164 probable transport
1445 71 3.9 277 2 T37424 probable 31.5K pro
1446 71 3.9 313 2 A34677 secretory pathway
1447 71 3.9 319 2 B53290 oligopeptide trans
1448 71 3.9 323 2 B72224 conserved hypotet
1449 71 3.9 336 2 C83926 S-adenosylmethioni
1450 71 3.9 344 2 A69325 hypothetical prote
1451 71 3.9 356 2 T40041 hypothetical prote
1452 71 3.9 357 2 E86823 peptidoglycan synt
1453 71 3.9 368 2 G81289 UDPgalactopyranose
1454 71 3.9 375 2 H86938 conserved hypotet
1455 71 3.9 397 2 F96680 conserved hypotet
1456 71 3.9 400 2 T34363 hypothetical prote
1457 71 3.9 404 2 AF2225 hypothetical prote
1458 71 3.9 405 1 VGBEGF glycoprotein G pre
1459 71 3.9 429 2 AC1163 flagellar hook-ass
1460 71 3.9 431 2 H81738 probable sodium-tr
1461 71 3.9 440 2 J10144 interleukin-6 rece
1462 71 3.9 460 2 J10145 interleukin-6 rece
1463 71 3.9 462 2 S74579 carboxyl-terminal
1464 71 3.9 472 2 AH3353 serine-type D-Ala-
1465 71 3.9 476 2 T19786 hypothetical prote
1466 71 3.9 478 2 H86100 hypothetical prote
1467 71 3.9 482 2 AC0426 serine-type D-Ala-
1468 71 3.9 501 2 T13316 hypothetical prote
1469 71 3.9 503 2 T40650 hypothetical prote
1470 71 3.9 507 2 J01929 phosphoprotein - r
1471 71 3.9 516 2 F82070 2-Isopropylmalate
1472 71 3.9 522 2 E69116 conserved hypotet
1473 71 3.9 642 2 G69371 acetyl-CoA synthe
1474 71 3.9 646 2 T27899 hypothetical prote
1475 71 3.9 659 2 A85854 hypothetical prote
1476 71 3.9 660 2 A00661 protein-like prote
1477 71 3.9 695 2 S66662 protein-glutamine
1478 71 3.9 784 2 F97981 exoribonuclease R
1479 71 3.9 786 2 F95977 protein tyrosine k
1480 71 3.9 837 2 S43556 furin (EC 3.4.21.7
1481 71 3.9 848 2 T28055 hypothetical prote
1482 71 3.9 922 2 T40372 trp asp repeat pro
1483 71 3.9 946 1 A29550 methylenetetrahydr
1484 71 3.9 1015 2 A29550 nuclear protein HI
1485 71 3.9 1032 2 T83164 hypothetical prote
1486 71 3.9 1035 2 T23165 hypothetical prote
1487 71 3.9 1036 2 T05687 beta-galactosidase
1488 71 3.9 1057 2 T16676 hypothetical prote
1489 71 3.9 1081 2 T15692 hypothetical prote

1490 71 3.9 1144 2 A36968 Pl-like adhesin pr
1491 71 3.9 1145 2 T05573 hypothetical prote
1492 71 3.9 1152 2 AC1347 probable peptidogl
1493 71 3.9 1268 2 B99789 hemagglutinin/hemo
1494 71 3.9 1270 2 E85649 hypothetical prote
1495 71 3.9 1341 2 S09579 tail fiber protein
1496 71 3.9 1500 1 SYRTCA carbamoyl-phosphat
1497 71 3.9 1555 2 S38758 amyo-alpha-1,6-gl
1498 71 3.9 2062 2 G96602 probable receptor
1499 71 3.9 2163 2 S50675 pre-mRNA splicing
1500 71 3.9 2183 2 T42764 coagulation factor

ALIGNMENTS

RESULT 1
156551
neurotrophin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56551
R;Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J.L.
J. Neurosci. 15, 2141-2156, 1995
A;Title: Cloning of neurotrophin defines a new subfamily of differentially expressed neur
A;Reference number: I56551; MUID:95198094; PMID:7891157
A;Accession: I56551
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-344 <RES>
A;Cross-references: UNIPROT:Q62718; EMBL:U16945; NID:g755184; PIDN:AAA67445.1; PID:g7551
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
Query Match 90.8%; Score 1639.5; DB 2; Length 344;
Best Local Similarity 92.9%; Pred. No. 2.5e-113;
Matches 312; Conservative 9; Mismatches 12; Indels 3; Gaps 1;
QY 12 ISWAIFTGLAALCLF---QGVPRSGDATFPKAMDNVTVRQESATLCTIDNRTVRVAV 68
Db 9 LPWKCLVVSRLLFLPTGTVPRSGDATFPKAMDNVTVRQESATLCTIDNRTVRVAV 68
QY 69 LNRSTILYAGNDKRWCLDPVRVLLSNTQYSIEIQNVDDVYDEGPTCSVQTDNHPKTSRV 128
Db 69 LNRSTILYAGNDKRWCLDPVRVLLSNTQYSIEIQNVDDVYDEGPTCSVQTDNHPKTSRV 128
QY 129 HLIQVSPKIVEISSDISINEGNNISLTCTATGPEPTVTRHISPKAVGVSEDEYLEI 188
Db 129 HLIQVSPKIVEISSDISINEGNNISLTCTATGPEPTVTRHISPKAVGVSEDEYLEI 188
QY 189 QGITREOSGDYECASNDVAAPVVRVKVTNVYPPYISEAKGTGVPVQKGTQCEASAV 248
Db 189 QGITREOSGDYECASNDVAAPVVRVKVTNVYPPYISEAKGTGVPVQKGTQCEASAV 248
QY 249 PSABFQWKDKRLIEGKKGKVKVKNRPFLSKLIFPNVSEHDYGNVTCVSNKLGHNTASI 308
Db 249 PSABFQWKDKRLIEGKKGKVKVKNRPFLSKLIFPNVSEHDYGNVTCVSNKLGHNTASI 308
QY 309 MLFGPGAVSEVNGTSRRAGCVWLLPLLVLLHLLKF 344
Db 309 MLFGPGAVSEVNGTSRRAGCVWLLPLLVLLHLLKF 344
RESULT 2
JC1238
opioid-binding protein (clone DUZ1) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: JC1238
R;Lippman, D.A.; Lee, N.M.; Loh, H.H.
Gene 117, 249-254, 1992
A;Title: Opioid-binding cell adhesion molecule (OBCAM)-related clones from a rat brain
A;Reference number: JC1238; MUID:92347701; PMID:1339369
A;Accession: JC1238

1271	72.5	4.0	676	2	F69276	conserved hypother	1344	72	4.0	992	2	T46337	hypothetical prote
1272	72.5	4.0	736	2	D96830	probable heat-shoc	1345	72	4.0	1076	1	A35622	nuclear pore prote
1273	72.5	4.0	759	1	B60008	RNA-directed RNA p	1346	72	4.0	1083	2	S48460	probable membrane
1274	72.5	4.0	836	2	A69550	hypothetical prote	1347	72	4.0	1106	2	A97647	cation efflux syst
1275	72.5	4.0	887	1	IUCHCL	E-cadherin precurs	1348	72	4.0	1106	2	AG2870	Acr family transpo
1276	72.5	4.0	894	2	S61015	hypothetical prote	1349	72	4.0	1132	2	H90834	host specificity p
1277	72.5	4.0	941	2	F97353	uncharacterized co	1350	72	4.0	1149	2	T27567	hypothetical prote
1278	72.5	4.0	954	2	S57108	hypothetical prote	1351	72	4.0	1155	2	H71456	probable pyrolysin
1279	72.5	4.0	970	2	I78842	receptor protein-t	1352	72	4.0	1199	2	S77082	pyruvate (flavodox
1280	72.5	4.0	1039	2	T15885	hypothetical prote	1353	72	4.0	1245	1	VH0VB2	structural polypro
1281	72.5	4.0	1166	2	T29009	hypothetical prote	1354	72	4.0	1391	2	S50608	hypothetical prote
1282	72.5	4.0	1186	2	T42729	histocompatibility	1355	72	4.0	1408	2	H69068	cell surface glyco
1283	72.5	4.0	1212	2	T42387	histocompatibility	1356	72	4.0	2094	2	S33124	tpz protein - huma
1284	72.5	4.0	1228	2	G90581	hypothetical prote	1357	72	4.0	2567	2	A49551	filamin, Muller ce
1285	72.5	4.0	1229	2	T25697	hypothetical prote	1358	72	4.0	2902	2	C71953	toxin-like outer m
1286	72.5	4.0	1276	2	B86546	polymorphic oute	1359	72	4.0	3890	2	C89921	hypothetical prote
1287	72.5	4.0	1276	2	C81591	polymorphic membra	1360	72	4.0	8563	2	T30226	polyketide synthas
1288	72.5	4.0	1306	2	S24624	aggregation protei	1361	71.5	4.0	91	2	S17628	ig kappa chain V r
1289	72.5	4.0	1383	2	T13052	guanine nucleotide	1362	71.5	4.0	119	2	PH1503	ig heavy chain V r
1290	72.5	4.0	1431	2	A15866	dextranucrase (BC	1363	71.5	4.0	121	2	S44113	ig heavy chain V r
1291	72.5	4.0	1500	1	JQ1348	carbamoyl-phosphat	1364	71.5	4.0	129	2	S40347	ig kappa chain - h
1292	72.5	4.0	1665	2	T29008	hypothetical prote	1365	71.5	4.0	225	2	JI0029	ig kappa chain pre
1293	72.5	4.0	1866	2	T08991	hypothetical prote	1366	71.5	4.0	246	1	A32999	myelin P0 protein
1294	72.5	4.0	2004	2	F95133	immunoglobulin A1	1367	71.5	4.0	275	2	H35216	FP31 protein - fow
1295	72.5	4.0	2052	2	C97038	phage-related prot	1368	71.5	4.0	275	2	C82752	hypothetical prote
1296	72.5	4.0	324	2	S37431	ankyrin 2, neurona	1369	71.5	4.0	290	2	T40852	cystathionine beta
1297	72.5	4.0	4845	2	T31067	BIR repeat contain	1370	71.5	4.0	303	2	H71693	hypothetical prote
1298	72	4.0	115	1	KVMSK2	ig kappa chain pre	1371	71.5	4.0	305	2	B84113	hypothetical prote
1299	72	4.0	115	2	A30995	T-cell receptor be	1372	71.5	4.0	321	2	F71163	probable oligopept
1300	72	4.0	131	2	B34904	ig kappa chain pre	1373	71.5	4.0	325	2	H90269	hypothetical prote
1301	72	4.0	131	2	B30577	ig kappa chain pre	1374	71.5	4.0	326	1	G2HU	ig gamma-2 chain C
1302	72	4.0	133	2	I45927	membrane-bound imm	1375	71.5	4.0	340	2	S20879	homeotic protein H
1303	72	4.0	148	2	PH0121	ig heavy chain pre	1376	71.5	4.0	360	2	H95980	probable uroporphyr
1304	72	4.0	148	2	PH0119	ig heavy chain pre	1377	71.5	4.0	361	2	S78542	dbpGlucose 4, 6-de
1305	72	4.0	208	1	WNV15	18.5K protein - Au	1378	71.5	4.0	384	2	A12962	cellulose synthesi
1306	72	4.0	223	2	I46696	CTLA-4 precursor -	1379	71.5	4.0	389	2	E58320	hypothetical prote
1307	72	4.0	239	2	F81795	probable periplasm	1380	71.5	4.0	476	2	A46118	myosin-binding pro
1308	72	4.0	338	2	A53066	CCAAT enhancer-bin	1381	71.5	4.0	477	2	JC4386	adenyl cyclase-a
1309	72	4.0	340	2	T02639	G5 protein homolog	1382	71.5	4.0	493	2	S39299	hexon protein - hu
1310	72	4.0	349	2	F70357	lipoprotein - Aqu	1383	71.5	4.0	507	1	A43387	polymerase-associa
1311	72	4.0	351	2	JQ2166	spindle body prote	1384	71.5	4.0	507	2	AC3036	glycerol-3-phospha
1312	72	4.0	372	1	UHRUCN	ciliary neurotroph	1385	71.5	4.0	507	2	H98249	glp gene homolog
1313	72	4.0	375	2	A64398	hypothetical prote	1386	71.5	4.0	520	2	A13295	adenylosuccinate s
1314	72	4.0	386	2	E84562	probable Tub fami	1387	71.5	4.0	523	1	S48997	IMP dehydrogenase
1315	72	4.0	411	1	VGBEG2	glycoprotein G pre	1388	71.5	4.0	572	2	B46529	ig V heavy chain (
1316	72	4.0	411	2	A37755	xylanase (EC 3.2.1	1389	71.5	4.0	592	2	JC4642	purH bifunctional
1317	72	4.0	424	2	H96963	dihydroorotase [im	1390	71.5	4.0	608	2	T32708	hypothetical prote
1318	72	4.0	425	2	AC2959	Hyd family secret	1391	71.5	4.0	611	2	T45493	glutamine-fructose
1319	72	4.0	428	2	T08626	sarcosine reductas	1392	71.5	4.0	647	2	F70057	penicillin-binding
1320	72	4.0	430	2	T32055	hypothetical prote	1393	71.5	4.0	659	2	S36551	E1 protein - human
1321	72	4.0	433	2	S76485	hypothetical prote	1394	71.5	4.0	668	2	T44118	penicillin-binding
1322	72	4.0	441	2	AF0048	modification methy	1395	71.5	4.0	668	2	JQ0774	phosphoribosylform
1323	72	4.0	452	2	C98324	hypothetical prote	1396	71.5	4.0	751	2	A13392	phosphoribosylform
1324	72	4.0	454	2	A46532	ig mu chain C regi	1397	71.5	4.0	775	1	I37422	glutamine-tRNA lig
1325	72	4.0	513	2	D96943	probable polygalac	1398	71.5	4.0	775	2	A32494	transposable eleme
1326	72	4.0	515	2	AH2996	glycerol-3-phospha	1399	71.5	4.0	776	2	S59790	hypothetical prote
1327	72	4.0	531	2	A98287	glp gene homolog	1400	71.5	4.0	860	2	AC0582	leucyl-tRNA synthet
1328	72	4.0	531	2	T50964	related to RCL1 pr	1401	71.5	4.0	893	2	F86476	protein F1504.39 l
1329	72	4.0	570	2	A57535	intrileukin 1 recep	1402	71.5	4.0	928	2	C97728	hypothetical prote
1330	72	4.0	570	2	T42621	hypothetical prote	1403	71.5	4.0	958	2	S32435	Na+/Ca2+-exchangin
1331	72	4.0	574	2	E64414	hypothetical prote	1404	71.5	4.0	1021	2	T15765	hypothetical prote
1332	72	4.0	576	2	G81657	DNA mismatch repai	1405	71.5	4.0	1025	2	T10259	RNA-directed DNA p
1333	72	4.0	627	2	S14683	ig mu chain precu	1406	71.5	4.0	1031	2	D88912	protein T06A10.1 l
1334	72	4.0	665	2	F97032	beta-glucosidase f	1407	71.5	4.0	1031	2	T33655	hypothetical prote
1335	72	4.0	697	2	T27587	hypothetical prote	1408	71.5	4.0	1094	2	S22573	DNA-directed DNA p
1336	72	4.0	777	1	TVVFCP	large T antigen -	1409	71.5	4.0	1125	2	H67644	TonB-dependent rec
1337	72	4.0	782	2	S22560	large T antigen -	1410	71.5	4.0	1128	1	T08322	plasmid replicatio
1338	72	4.0	844	2	T37690	hypothetical prote	1411	71.5	4.0	1231	2	S30185	insulin receptor s
1339	72	4.0	844	2	T52396	formin-binding pro	1412	71.5	4.0	1250	2	T40062	probable nuclear e
1340	72	4.0	868	2	D86349	hypothetical prote	1413	71.5	4.0	1441	2	T13717	CRAG protein - fru
1341	72	4.0	878	1	RXSBIB	RNA-directed RNA p	1414	71.5	4.0	1446	2	S73013	polyketide synthas
1342	72	4.0	892	2	T06818	DNA topoisomerase	1415	71.5	4.0	1448	2	A12007	Subtilase family p
1343	72	4.0	984	2	C84781	hypothetical prote	1416	71.5	4.0	1526	2	AC2239	WD-40 repeat prote

1125	74	4.1	879	2	H64888	membrane protein y	1198	73	4.0	469	2	D95989	conserved hypothet
1126	74	4.1	908	2	T25035	hypothetical prote	1199	73	4.0	478	2	S47040	Gene Tc52 protein
1127	74	4.1	966	2	E87473	TonB-dependent rec	1200	73	4.0	481	2	C97238	ATP dependent RNA
1128	74	4.1	1085	2	JC2227	probable helicase	1201	73	4.0	523	2	A12696	serine proteinase
1129	74	4.1	1128	2	H90538	hypothetical prote	1202	73	4.0	523	2	A12696	probable serine pr
1130	74	4.1	1132	1	QSBPL	host specificity p	1203	73	4.0	565	2	H69342	GTP-binding protei
1131	74	4.1	1136	1	S57845	protein-tyrosine k	1204	73	4.0	586	2	T45945	laccase-like prote
1132	74	4.1	1137	2	B90734	probable host spec	1205	73	4.0	657	2	A1525	probable cell surf
1133	74	4.1	1482	2	S13495	pregnancy zone pro	1206	73	4.0	671	2	T23015	hypothetical prote
1134	74	4.1	1488	2	C70984	probable ppsE prot	1207	73	4.0	673	2	H86761	glycine-tRNA ligas
1135	74	4.1	1524	2	A69590	DNA segregation AR	1208	73	4.0	673	2	T41768	ACMNPV orf23 - Bom
1136	74	4.1	1963	2	B98002	IGA-specific metal	1209	73	4.0	688	2	S39491	prochlorophyllid
1137	74	4.1	2185	1	GNNYSH	genome polyprotein	1210	73	4.0	701	2	H95039	hypothetical prote
1138	74	4.1	2812	2	T43271	phosphotidylinosit	1211	73	4.0	722	2	D70200	polyribonucleotide
1139	73.5	4.1	64	2	S20961	keratinocyte growt	1212	73	4.0	745	2	B33856	hypothetical 80K p
1140	73.5	4.1	96	2	PH1070	Ig light chain V r	1213	73	4.0	754	2	E86592	general secretion
1141	73.5	4.1	97	2	S26341	Ig light chain V r	1214	73	4.0	754	2	D72032	general secretion
1142	73.5	4.1	119	2	PH1510	Ig heavy chain V r	1215	73	4.0	771	2	AF2056	cation transportin
1143	73.5	4.1	119	2	PH1518	Ig heavy chain V r	1216	73	4.0	772	2	A46108	outer capsid prote
1144	73.5	4.1	133	2	PC1155	Ig heavy chain pre	1217	73	4.0	858	2	T12142	lipoxigenase (EC 1
1145	73.5	4.1	135	2	PH1493	Ig heavy chain V r	1218	73	4.0	870	2	T47454	lipoxigenase AtLOX
1146	73.5	4.1	140	2	PH1486	Ig heavy chain V r	1219	73	4.0	896	2	JQ2391	hypothetical prote
1147	73.5	4.1	140	2	PH1486	Ig heavy chain V r	1220	73	4.0	897	2	S67283	hypothetical prote
1148	73.5	4.1	229	2	A20969	Ig kappa chain pre	1221	73	4.0	935	2	S66306	valine-tRNA ligase
1149	73.5	4.1	309	2	T09564	glutaminyl-peptide	1222	73	4.0	980	2	T39630	hypothetical prote
1150	73.5	4.1	339	2	T28138	Ig V-region-like B	1223	73	4.0	1095	2	T24061	hypothetical prote
1151	73.5	4.1	340	2	T28137	Ig V-region-like B	1224	73	4.0	1336	2	T18288	ABC transport prot
1152	73.5	4.1	366	2	AF0497	DNA-directed DNA p	1225	73	4.0	1473	2	A35186	salivary agglutini
1153	73.5	4.1	380	2	S12839	Ig heavy chain pre	1226	73	4.0	1518	2	T28880	hypothetical prote
1154	73.5	4.1	388	2	E95007	sugar isomerase do	1227	73	4.0	1815	2	B95942	conserved hypothet
1155	73.5	4.1	400	2	T28853	probable cathepsin	1228	73	4.0	2207	2	S09553	genome polyprotein
1156	73.5	4.1	418	2	G87469	Th13/fpfi family p	1229	73	4.0	2210	1	R3PVT	genome polyprotein
1157	73.5	4.1	422	2	A96912	glutamate-l-semial	1230	73	4.0	2907	2	A57278	fibrillin-2 precur
1158	73.5	4.1	431	2	S37775	filamin, muscle -	1231	73	4.0	3011	1	S40770	genome polyprotein
1159	73.5	4.1	505	2	AC3486	cell surface prote	1232	73	4.0	3263	2	E82410	hypothetical prote
1160	73.5	4.1	579	2	B49256	cell division prot	1233	73	4.0	4688	2	F82885	hypothetical prote
1161	73.5	4.1	632	2	C98264	5'-nucleotidase pr	1234	73	4.0	4936	2	AH2515	hypothetical prote
1162	73.5	4.1	636	2	AE3020	5'-nucleotidase [i	1235	72.5	4.0	124	2	S40364	Ig kappa chain - h
1163	73.5	4.1	677	2	T04145	probable beta-adap	1236	72.5	4.0	126	2	S40312	Ig kappa chain - h
1164	73.5	4.1	725	2	C87485	ComEC/Rec2 family	1237	72.5	4.0	128	2	S20636	Ig kappa chain v r
1165	73.5	4.1	815	2	E70021	3-hydroxyacyl-CoA	1238	72.5	4.0	137	2	E34903	Ig heavy chain pre
1166	73.5	4.1	941	2	S29043	cellulase (EC 3.2.	1239	72.5	4.0	141	2	I47178	Ig heavy chain var
1167	73.5	4.1	986	2	B1675	polymorphic membra	1240	72.5	4.0	198	2	T19797	hypothetical prote
1168	73.5	4.1	1005	2	T18537	Ig heavy chain - c	1241	72.5	4.0	199	2	G75153	hypothetical prote
1169	73.5	4.1	1052	2	H83909	cell wall-associat	1242	72.5	4.0	215	2	I64004	hypothetical prote
1170	73.5	4.1	1119	2	A86340	protein F2D10.24 [1243	72.5	4.0	219	2	S38865	Ig kappa chain - m
1171	73.5	4.1	1121	2	I38127	phosphoprotein pho	1244	72.5	4.0	233	1	JU0284	Fc gamma (IgG) rec
1172	73.5	4.1	1280	2	T00365	hypothetical prote	1245	72.5	4.0	247	2	P00655	outer capsid spike
1173	73.5	4.1	1285	2	B72420	hypothetical prote	1246	72.5	4.0	247	2	P00656	outer capsid spike
1174	73.5	4.1	1292	2	T09229	galactose binding	1247	72.5	4.0	247	2	P00657	outer capsid spike
1175	73.5	4.1	1330	1	GPFFE	epidermal growth f	1248	72.5	4.0	264	2	F27579	T-cell receptor al
1176	73.5	4.1	1487	2	S15904	alpha-1 proteinase	1249	72.5	4.0	267	2	PL0084	T-cell receptor be
1177	73.5	4.1	1571	2	T00062	hypothetical prote	1250	72.5	4.0	286	2	S32480	hypothetical prote
1178	73.5	4.1	3328	2	T30835	breast cancer tumo	1251	72.5	4.0	288	2	S29690	Ig heavy chain VDJ
1179	73	4.0	126	2	S24704	Ig heavy chain V6	1252	72.5	4.0	289	2	G00031	B7 protein - red-c
1180	73	4.0	127	2	PH1224	Ig kappa chain pre	1253	72.5	4.0	312	2	D82690	adenine-specific m
1181	73	4.0	128	2	PH0445	Ig kappa chain pre	1254	72.5	4.0	322	2	T50167	hypothetical prote
1182	73	4.0	131	2	E25733	T-cell receptor al	1255	72.5	4.0	350	2	T21106	hypothetical prote
1183	73	4.0	132	2	A27632	T-cell receptor al	1256	72.5	4.0	377	2	T05453	trehalose-6-phosph
1184	73	4.0	133	1	K4HUJI	Ig kappa chain pre	1257	72.5	4.0	401	2	E87531	hypothetical prote
1185	73	4.0	145	2	S21651	T-cell receptor be	1258	72.5	4.0	408	2	D95417	probable ABC trans
1186	73	4.0	225	2	E82473	hypothetical prote	1259	72.5	4.0	423	2	F64436	adenosylmethionine
1187	73	4.0	233	2	S25747	Ig lambda chain -	1260	72.5	4.0	428	2	B84984	hypothetical prote
1188	73	4.0	332	2	G83458	sulfate-binding pr	1261	72.5	4.0	451	2	T48340	hypothetical prote
1189	73	4.0	349	2	T08782	hypothetical prote	1262	72.5	4.0	453	2	C31933	Ig mu chain C regi
1190	73	4.0	389	2	B42708	serine-type D-Ala-	1263	72.5	4.0	475	2	S01321	Ig gamma-2b chain
1191	73	4.0	393	1	HVRKC1	Ig mu chain C regi	1264	72.5	4.0	482	2	T49079	serine-type carbox
1192	73	4.0	438	1	HVRKC2	Ig mu chain C regi	1265	72.5	4.0	498	2	G97279	protein containing
1193	73	4.0	445	2	S67695	26S proteasome reg	1266	72.5	4.0	503	2	B72289	oligopeptide ABC t
1194	73	4.0	451	1	S75239	hypothetical prote	1267	72.5	4.0	527	2	T22000	hypothetical prote
1195	73	4.0	454	2	AE1970	hypothetical prote	1268	72.5	4.0	533	2	A42249	aspartic proteinas
1196	73	4.0	469	1	P2WL35	L2 protein - human	1269	72.5	4.0	560	2	B81451	flagellar M-ring p
1197	73	4.0	469	2	S36525	L2 protein - human	1270	72.5	4.0	668	2	T05803	hypothetical prote

979	75.5	4.2	132	2	PH0106	anti-digoxin trans	1052	75	4.2	1311	2	T33757	hypothetical prote
980	75.5	4.2	133	2	S40324	Ig kappa chain v r	1053	75	4.2	1313	2	G82887	hypothetical prote
981	75.5	4.2	140	1	HVMSG7	Ig heavy chain pr	1054	75	4.2	1476	2	AC2220	hypothetical prote
982	75.5	4.2	140	2	PH1489	Ig heavy chain v r	1055	75	4.2	1661	2	H71439	hypothetical prote
983	75.5	4.2	189	2	T39849	anaphase promoting	1056	75	4.2	1672	2	T46237	hypothetical prote
984	75.5	4.2	231	2	PC4155	Ig gamma-2b chain	1057	75	4.2	2291	2	S11238	polymyrase - Berne
985	75.5	4.2	234	2	A39956	Ig lambda chain pr	1058	75	4.2	2413	2	S34670	splicing factor PR
986	75.5	4.2	248	2	F96655	hypothetical prote	1059	75	4.2	2500	2	G71609	hypothetical prote
987	75.5	4.2	249	2	G69081	acetyl-CoA synthet	1060	74.5	4.1	116	1	HVMS1B	Ig heavy chain v r
988	75.5	4.2	262	2	T42986	v-cyclin - ateline	1061	74.5	4.1	119	2	PH1517	Ig heavy chain v r
989	75.5	4.2	316	2	F86157	hypothetical prote	1062	74.5	4.1	119	2	PH1516	Ig heavy chain v r
990	75.5	4.2	341	2	S72445	DNA-binding protei	1063	74.5	4.1	140	2	PH1488	hypothetical prote
991	75.5	4.2	362	2	S16303	polygalacturonase	1064	74.5	4.1	192	2	T02893	hypothetical prote
992	75.5	4.2	398	2	T46475	hypothetical prote	1065	74.5	4.1	232	2	S25756	Ig lambda chain -
993	75.5	4.2	402	2	F70850	DNA-directed DNA p	1066	74.5	4.1	243	2	AC3071	transcription regu
994	75.5	4.2	504	2	S00390	Ig gamma chain (cl	1067	74.5	4.1	277	2	S29922	Sal18L protein pre
995	75.5	4.2	524	2	D87440	2-isopropylmalate	1068	74.5	4.1	370	1	HVRKCS	Ig mu chain C regi
996	75.5	4.2	569	2	A48462	T cell activation	1069	74.5	4.1	397	2	S70987	dnaN protein - Myc
997	75.5	4.2	580	2	S49308	beta-fructofuranos	1070	74.5	4.1	438	2	B97712	hypothetical prote
998	75.5	4.2	582	2	S53814	DEAD box protein -	1071	74.5	4.1	466	1	SYECNT	asparagine-tRNA li
999	75.5	4.2	641	2	JC7142	dextranase (EC 3.2	1072	74.5	4.1	468	1	P2WL51	L2 protein - human
1000	75.5	4.2	691	1	S46735	NADPH-ferrihemopro	1073	74.5	4.1	501	2	S74341	hypothetical prote
1001	75.5	4.2	710	1	A48273	mitochondrial inte	1074	74.5	4.1	549	2	S04845	Ig heavy chain pre
1002	75.5	4.2	713	1	ALBSG7	cyclomaltodextrin	1075	74.5	4.1	591	1	CBY12	L-lactate dehydrog
1003	75.5	4.2	739	2	A55314	glycine-tRNA ligas	1076	74.5	4.1	644	2	S50552	hypothetical prote
1004	75.5	4.2	746	2	E64701	conserved hypotet	1077	74.5	4.1	663	2	AG0782	colicin I receptor
1005	75.5	4.2	771	2	B70564	hypothetical prote	1078	74.5	4.1	693	2	UN0843	heat shock protein
1006	75.5	4.2	815	2	AB2444	hypothetical prote	1079	74.5	4.1	729	2	T46270	hypothetical prote
1007	75.5	4.2	857	1	S05943	gelation factor -	1080	74.5	4.1	807	2	T39479	histone transcript
1008	75.5	4.2	918	2	D71407	hypothetical prote	1081	74.5	4.1	862	2	E88594	protein Y48A85.11
1009	75.5	4.2	1068	2	S73091	hypothetical prote	1082	74.5	4.1	899	2	A83019	conserved hypotet
1010	75.5	4.2	1787	2	A92973	hypothetical prote	1083	74.5	4.1	947	2	T26314	hypothetical prote
1011	75.5	4.2	1818	2	AE3011	conserved hypotet	1084	74.5	4.1	1043	2	D84900	hypothetical prote
1012	75.5	4.2	1871	2	D96698	probable DNA polym	1085	74.5	4.1	1183	2	S63046	probable membrane
1013	75.5	4.2	1894	2	T02155	DNA-directed DNA p	1086	74.5	4.1	1403	2	T11583	probable translati
1014	75.5	4.2	2265	1	FNBO	fibronectin - bovi	1087	74.5	4.1	1622	2	T45240	hypothetical prote
1015	75.5	4.2	5005	2	F82884	hypothetical prote	1088	74.5	4.1	1825	2	S13507	microtubule-associ
1016	75.5	4.2	6669	2	S55024	nebulin, skeletal	1089	74.5	4.1	1830	2	A37981	microtubule-associ
1017	75	4.2	1066	2	A49138	IGA kappa rheumato	1090	74.5	4.1	2338	2	I73957	kinase-related pro
1018	75	4.2	115	2	B26524	T-cell receptor be	1091	74.5	4.1	2366	2	S10317	toxin B - Clostrid
1019	75	4.2	117	2	S40362	Ig kappa chain - h	1092	74.5	4.1	2761	2	T21064	hypothetical prote
1020	75	4.2	128	2	A47159	Ig lambda chain v	1093	74.5	4.1	2761	2	S79908	hypothetical 527K
1021	75	4.2	131	2	D29380	Ig kappa chain pre	1094	74.5	4.1	4639	1	A54794	Ig kappa chain v r
1022	75	4.2	130	2	C34904	Ig heavy chain pre	1095	74	4.1	107	2	S12954	hypothetical prote
1023	75	4.2	148	2	PH0115	Ig heavy chain pre	1096	74	4.1	108	2	T26681	Ig kappa chain v r
1024	75	4.2	157	2	D31327	IGF receptor alpha	1097	74	4.1	131	2	S52449	Ig kappa chain v r
1025	75	4.2	215	2	A57843	sodium channel bet	1098	74	4.1	196	2	S72716	4-coumarate-CoA li
1026	75	4.2	246	2	E69230	hypothetical prote	1099	74	4.1	221	1	QBE48	BARF1 protein - hu
1027	75	4.2	268	2	A56446	Ig heavy chain v r	1100	74	4.1	231	2	S25751	Ig lambda chain -
1028	75	4.2	283	2	AH1767	protoporphyrinogen	1101	74	4.1	248	2	B45831	MHC class I histoc
1029	75	4.2	285	2	B82842	spermidine synthas	1102	74	4.1	277	2	D42521	MHC class I histoc
1030	75	4.2	297	2	AC2380	hypothetical prote	1103	74	4.1	365	2	I37476	HLA-A30.3 precurs
1031	75	4.2	307	1	RWMSBC	T-cell receptor be	1104	74	4.1	365	2	I56039	MHC class I histoc
1032	75	4.2	321	2	S10006	hypothetical prote	1105	74	4.1	365	2	I38519	transcription fact
1033	75	4.2	359	2	AF3184	beta-lactamase (im	1106	74	4.1	416	1	A41267	flagellar hook-ass
1034	75	4.2	364	2	S03535	class I histocompa	1107	74	4.1	429	2	AC1522	Ig mu chain C regi
1035	75	4.2	392	2	T34095	zinc finger protei	1108	74	4.1	438	1	HVRKCS	hemolysin - Helic
1036	75	4.2	393	2	T03216	enoyl-lacyl-carrie	1109	74	4.1	449	2	B64706	hypothetical prote
1037	75	4.2	394	2	G69230	endo-1,4-beta-gluc	1110	74	4.1	454	2	T26296	Ig mu chain C regi
1038	75	4.2	416	2	E64140	hypothetical prote	1111	74	4.1	461	1	HVRKCO	transcription fact
1039	75	4.2	435	2	T42613	probable envelope	1112	74	4.1	468	1	TWMS2	hypothetical prote
1040	75	4.2	439	2	G97159	contains cell adhe	1113	74	4.1	474	2	T47299	hypothetical prote
1041	75	4.2	444	2	B90053	hypothetical prote	1114	74	4.1	514	2	G89903	conserved hypotet
1042	75	4.2	476	2	S64291	hypothetical prote	1115	74	4.1	523	2	F9638	2-isopropylmalate
1043	75	4.2	479	1	VGBEF2	glycoprotein F - h	1116	74	4.1	523	2	B64729	2-isopropylmalate
1044	75	4.2	535	2	S76564	hypothetical prote	1117	74	4.1	523	2	B4729	hypothetical prote
1045	75	4.2	574	2	T29005	hypothetical prote	1118	74	4.1	562	2	AH2084	laccase (EC 1.10.3
1046	75	4.2	577	2	I50731	Ig heavy chain - n	1119	74	4.1	573	2	T02743	probable acyl-CoA
1047	75	4.2	701	2	C97910	ATP-dependent prot	1120	74	4.1	579	2	D87063	hypothetical prote
1048	75	4.2	743	2	T34853	probable fusidic a	1121	74	4.1	587	2	S63033	hypothetical prote
1049	75	4.2	775	1	JQ1639	outer layer protei	1122	74	4.1	701	2	C97302	hypothetical prote
1050	75	4.2	780	2	T31548	hypothetical prote	1123	74	4.1	755	2	T48553	subtilisin-like pr
1051	75	4.2	1242	1	DJBEC1	DNA-directed DNA p	1124	74	4.1	876	2	T51507	WD40-repeat protei

833	78	4.3	301	1	G64491	thioredoxin-disulf	906	76.5	4.2	267	1	RWMS8	T-cell receptor al
834	78	4.3	320	1	I47158	Ig gamma 1 chain c	907	76.5	4.2	299	1	AHRB	Ig alpha chain C r
835	78	4.3	370	1	HLHUA3	MHC class I histoc	908	76.5	4.2	306	1	B75129	thiamin biosynthes
836	78	4.3	413	2	AG3267	amino-acid N-acety	909	76.5	4.2	332	2	D83745	3-oxoacyl-lacyl-ca
837	78	4.3	460	2	S67174	hypothetical prote	910	76.5	4.2	408	2	S53477	IMP dehydrogenase
838	78	4.3	475	2	T44566	conserved hypoteth	911	76.5	4.2	428	2	AH3536	dihydroliipoamide S
839	78	4.3	831	2	E82217	asparaginyl-tRNA s	912	76.5	4.2	431	2	A86601	hypothetical prote
840	78	4.3	542	2	A84554	hypothetical prote	913	76.5	4.2	431	2	G72022	probable sodium-tr
841	78	4.3	702	2	T21148	hypothetical prote	914	76.5	4.2	457	2	A27449	T-cell surface gly
842	78	4.3	874	2	C84513	Mutator-like trans	915	76.5	4.2	463	2	T14884	hypothetical prote
843	78	4.3	980	2	H90681	probable flagellin	916	76.5	4.2	483	2	A69745	hypothetical prote
844	78	4.3	980	2	D85532	probable structura	917	76.5	4.2	515	2	H86202	hypothetical prote
845	78	4.3	1016	2	H71460	probable outer mem	918	76.5	4.2	516	2	E70035	levanase homolog y
846	78	4.3	1029	2	F96602	hypothetical prote	919	76.5	4.2	528	2	PC4025	intercellular adhe
847	78	4.3	1138	1	S24066	protein-tyrosine k	920	76.5	4.2	547	2	S75904	hypothetical prote
848	78	4.3	1217	2	F97177	alpha-glucosidase	921	76.5	4.2	563	2	T20631	hypothetical prote
849	78	4.3	2185	1	GNYSV	genome polyprotein	922	76.5	4.2	572	1	HNNZB3	hemagglutinin-neur
850	78	4.3	2256	2	AD1018	large repetitive p	923	76.5	4.2	573	2	F89719	protein F09B12.1 {
851	78	4.3	4302	2	A38971	polycystic kidney	924	76.5	4.2	573	2	T20632	hypothetical prote
852	77.5	4.3	119	2	PH1519	Ig heavy chain V r	925	76.5	4.2	622	2	A36915	fructanase - Bacte
853	77.5	4.3	140	2	A36194	Ig heavy chain V r	926	76.5	4.2	653	2	B90908	probable host spec
854	77.5	4.3	284	2	S75817	hypothetical prote	927	76.5	4.2	656	2	B71290	conserved hypoteth
855	77.5	4.3	307	2	C71002	hypothetical prote	928	76.5	4.2	740	2	AD0485	probable exported
856	77.5	4.3	309	2	T15747	hypothetical prote	929	76.5	4.2	749	2	E86774	hypothetical prote
857	77.5	4.3	315	1	HNZVVT	hemagglutinin prec	930	76.5	4.2	775	2	G90996	probable host spec
858	77.5	4.3	428	2	T48167	hypothetical prote	931	76.5	4.2	782	2	A85693	hypothetical prote
859	77.5	4.3	446	2	S40295	Ig gamma-2a chain	932	76.5	4.2	896	2	T22061	hypothetical prote
860	77.5	4.3	466	2	C85619	asparagine tRNA sy	933	76.5	4.2	913	2	E75554	valyl-tRNA synthet
861	77.5	4.3	466	2	E90755	asparagine tRNA sy	934	76.5	4.2	1039	2	T30856	protein F2 - Strep
862	77.5	4.3	469	1	TVHUE2	transcription fact	935	76.5	4.2	1124	1	I58388	protein-tyrosine k
863	77.5	4.3	532	2	C42804	immunodominant typ	936	76.5	4.2	1131	2	T14517	hypothetical prote
864	77.5	4.3	534	2	S60205	phosphonoacetaldeh	937	76.5	4.2	1151	2	S48431	probable membrane
865	77.5	4.3	584	2	F70522	probable polyketid	938	76.5	4.2	1248	2	C98874	autolysin [importe
866	77.5	4.3	593	2	AI12319	internalin protein	939	76.5	4.2	1363	2	C84346	hypothetical prote
867	77.5	4.3	655	2	T34219	hypothetical prote	940	76.5	4.2	1377	2	I54632	tsh protein - Esch
868	77.5	4.3	668	2	S49639	probable membrane	941	76.5	4.2	1648	2	S61654	probable membrane
869	77.5	4.3	676	2	T30480	envelope protein h	942	76.5	4.2	2477	2	S14428	fibronectin precur
870	77.5	4.3	852	1	VCLJGG	env polyprotein pr	943	76	4.2	91	2	PH1071	Ig light chain V r
871	77.5	4.3	888	2	A54280	cell differentiat	944	76	4.2	107	2	FD0011	Ig kappa chain V r
872	77.5	4.3	1192	2	T08609	hypothetical prote	945	76	4.2	108	2	G30560	Ig kappa chain V r
873	77.5	4.3	1474	2	F69009	probable membrane	946	76	4.2	108	2	S38720	Ig light chain V r
874	77.5	4.3	1515	2	A40203	4-alpha-glucanotra	947	76	4.2	118	2	I33932	Ig kappa chain pre
875	77.5	4.3	1819	2	D97033	uncharacterized pr	948	76	4.2	120	2	C29775	Ig kappa chain pre
876	77.5	4.3	1825	2	C98400	protein H19W22.1 {	949	76	4.2	161	2	S04931	T-cell receptor de
877	77.5	4.3	1825	2	T32828	hypothetical prote	950	76	4.2	251	2	S64927	probable membrane
878	77.5	4.3	3329	2	T42205	breast cancer susc	951	76	4.2	254	2	B75052	coenzyme pqg synch
879	77.5	4.3	3329	2	T30904	breast cancer tumo	952	76	4.2	310	2	F90011	conserved hypoteth
880	77.5	4.3	3591	1	S21010	filamentous hemagg	953	76	4.2	327	2	T07104	2'-hydroxydihydro
881	77	4.3	107	2	PC4405	Ig kappa chain V r	954	76	4.2	327	2	S06611	Ig gamma-2 chain C
882	77	4.3	128	2	S40343	Ig kappa chain V-J	955	76	4.2	365	2	D87526	hypothetical prote
883	77	4.3	234	2	S01320	Ig kappa chain pre	956	76	4.2	426	2	H84846	probable polygalac
884	77	4.3	302	2	S50579	hypothetical prote	957	76	4.2	430	2	T28143	tapasin 1 homolog
885	77	4.3	328	2	I47161	Ig gamma 3 chain c	958	76	4.2	431	2	F71476	probable sodium-tr
886	77	4.3	338	2	S09276	Ig alpha chain C r	959	76	4.2	450	1	MHDG	Ig mu chain C regi
887	77	4.3	384	2	E84871	probable polygalac	960	76	4.2	473	2	H83676	pyruvate dehydroge
888	77	4.3	439	2	A81251	probable peptidogl	961	76	4.2	501	2	E96509	protein F27F5_17 {
889	77	4.3	614	2	A88466	protein S0244.2 {l	962	76	4.2	506	1	ACRYG1	nicotinic acetylch
890	77	4.3	817	2	F86742	ribonuclease [limpo	963	76	4.2	511	2	E84685	probable seed stor
891	77	4.3	859	2	AC2089	adenylate cyclase	964	76	4.2	516	2	A44494	CAMP-responsive el
892	77	4.3	879	2	C90879	hypothetical prote	965	76	4.2	577	2	T48530	clathrin binding p
893	77	4.3	879	2	G85739	hypothetical prote	966	76	4.2	656	2	AC0429	2',3'-cyclic-nucle
894	77	4.3	928	2	A87749	protein F55C7.7c {	967	76	4.2	859	1	VCLJCT	env polyprotein pr
895	77	4.3	976	2	C96958	ACT domain contain	968	76	4.2	1020	2	A46405	C protein alpha an
896	77	4.3	1071	1	PXBYYA	H+-exporting ATPas	969	76	4.2	1151	2	S03722	DNA-directed DNA p
897	77	4.3	1176	2	A33856	surface-layer 125K	970	76	4.2	1196	2	H86389	hypothetical prote
898	77	4.3	2488	2	T42739	guanine nucleotide	971	76	4.2	1278	2	A47462	probable DNA-direc
899	77	4.3	3562	2	A47171	chondroitin sulfat	972	76	4.2	1366	2	S57664	IgA-specific metal
900	76.5	4.2	135	2	PH1492	Ig heavy chain V r	973	76	4.2	2380	2	T29551	hypothetical prote
901	76.5	4.2	136	2	A49137	Ig kappa chain pre	974	75.5	4.2	104	2	JC6076	anti-D-dimer monoc
902	76.5	4.2	178	2	S29594	Ig gamma chain (WM	975	75.5	4.2	114	2	S44119	Ig kappa chain V-J
903	76.5	4.2	232	2	S17399	Ig lambda chain (W	976	75.5	4.2	123	2	S35479	Ig kappa chain pre
904	76.5	4.2	236	2	A24637	T-cell surface gly	977	75.5	4.2	131	2	S09259	Ig kappa chain pre
905	76.5	4.2	252	2	AF2719	arginine-tRNA-prot	978	75.5	4.2	131	2	D29380	Ig kappa chain pre

687	82	4.5	663	1	QREIC	colicin I receptor	760	79.5	4.4	290	2	C97533	pyruvate dehydroge
688	82	4.5	820	2	T14879	hypothetical prote	761	79.5	4.4	306	2	A52752	pyruvate dehydroge
689	82	4.5	841	2	JC5894	killer cell inhibi	762	79.5	4.4	468	1	A41242	interleukin-6 rece
690	82	4.5	842	2	T04555	hypothetical prote	763	79.5	4.4	474	2	I50830	Ig mu chain - Lepi
691	82	4.5	1125	1	S57846	hypothetical prote	764	79.5	4.4	522	2	B42804	immunodominant typ
692	82	4.5	1222	1	T22490	protein-tyrosine k	765	79.5	4.4	558	2	A44964	apical membrane an
693	82	4.5	1577	2	T30858	glucosyltransferas	766	79.5	4.4	653	2	A49722	endoglin precursor
694	81.5	4.5	107	2	PL0268	Ig kappa chain v r	767	79.5	4.4	766	1	CDHU26	dipeptidyl-peptida
695	81.5	4.5	240	2	A41797	Ig kappa chain - s	768	79.5	4.4	1022	1	S00503	Na+/K+-exchanging
696	81.5	4.5	247	2	A34954	T-cell surface gly	769	79.5	4.4	1034	1	A53663	enteropeptidase [E
697	81.5	4.5	259	2	JC7109	ST2V protein - hum	770	79.5	4.4	1036	2	B93368	hypothetical prote
698	81.5	4.5	656	2	T23338	hypothetical prote	771	79.5	4.4	1156	2	T23308	hypothetical prote
699	81.5	4.5	1183	2	A89135	protein F25G6.2 [i	772	79.5	4.4	1185	2	A42404	collagen adhesin -
700	81.5	4.5	1203	2	S27545	pullulanase - Ther	773	79.5	4.4	1409	2	T42522	protein-tyrosine-p
701	81.5	4.5	1336	2	T17479	hypothetical prote	774	79.5	4.4	1422	2	T30111	hypothetical prote
702	81.5	4.5	1983	2	G86643	hypothetical prote	775	79	4.4	91	2	S17638	Ig kappa chain v r
703	81	4.5	234	2	S14237	Ig kappa chain pre	776	79	4.4	101	2	H57262	Ig heavy chain v r
704	81	4.5	247	2	A55717	myelin/oligodendro	777	79	4.4	231	2	S25753	Ig lambda chain -
705	81	4.5	314	1	HNZVW	hemagglutinin prec	778	79	4.4	348	2	C81284	cyathionine beta
706	81	4.5	314	1	JQ1793	hemagglutinin prec	779	79	4.4	370	2	G97001	endoglucanase fami
707	81	4.5	451	2	S71754	cellular hepatitis	780	79	4.4	387	2	T04322	polygalacturonase
708	81	4.5	545	2	A38447	oligonopeptide ABC t	781	79	4.4	403	2	T20727	hypothetical prote
709	81	4.5	568	2	A45804	Ig mu chain C regi	782	79	4.4	432	2	S30193	T-cell surface gly
710	81	4.5	571	2	H63584	acetolactate synth	783	79	4.4	450	2	B97292	probable ATP-depen
711	81	4.5	578	2	B96683	hypothetical prote	784	79	4.4	474	1	G2MS11	Ig gamma-2b chain
712	81	4.5	585	2	A46507	Ig alpha chain - c	785	79	4.4	659	2	G91009	colicin I receptor
713	81	4.5	588	2	C83836	subtilisin-type pr	786	79	4.4	753	2	G02173	semaphorin III fam
714	81	4.5	637	2	B83052	DnaK protein PA476	787	79	4.4	807	2	A71663	DNA gyrase chain B
715	81	4.5	665	2	E86775	ribonuclease limpo	788	79	4.4	875	2	H50371	proteinase [import
716	80.5	4.5	248	1	Q0BE4L	probable glycoprot	789	79	4.4	1175	2	D85089	hypothetical prote
717	80.5	4.5	269	2	B97501	hypothetical prote	790	79	4.4	1204	2	C75015	probable pyrolysin
718	80.5	4.5	273	2	G89856	conserved hypothe	791	79	4.4	1350	2	AF2005	RNA polymerase bet
719	80.5	4.5	277	2	I47162	Ig gamma 4 chain c	792	79	4.4	1439	2	T27110	hypothetical prote
720	80.5	4.5	298	2	T30086	hypothetical prote	793	78.5	4.3	111	2	D17266	Ig kappa chain v r
721	80.5	4.5	327	2	B97076	UDP-glucose 4-epim	794	78.5	4.3	115	2	B46518	Ig L1 chain v regi
722	80.5	4.5	358	2	A95214	SUA5 related conse	795	78.5	4.3	140	2	PH1498	Ig heavy chain v r
723	80.5	4.5	459	2	A46254	CD4 precursor - ra	796	78.5	4.3	228	2	S29575	Ig light chain - r
724	80.5	4.5	466	2	AF0616	asparagine-tRNA li	797	78.5	4.3	293	1	XYRBM	DNA repair protein
725	80.5	4.5	517	2	B76444	4-coumarate-CoA li	798	78.5	4.3	323	2	JC2578	arylamine N-acetyl
726	80.5	4.5	554	2	A91250	probable portal pr	799	78.5	4.3	373	2	JH0155	pectin lyase (EC 4
727	80.5	4.5	596	2	D84972	ABC transporter AT	800	78.5	4.3	392	2	T03229	enoyl-[acyl]-carrie
728	80.5	4.5	613	2	T41565	hypothetical prote	801	78.5	4.3	434	2	S72430	transcription elon
729	80.5	4.5	881	2	S67026	probable membrane	802	78.5	4.3	434	2	D88305	protein R03D7.4 [i
730	80.5	4.5	1025	2	G81722	polymorphic membra	803	78.5	4.3	553	1	SMEBH1	flagellar hook-ass
731	80.5	4.5	1128	1	T08312	plasmid replicatio	804	78.5	4.3	553	2	A40640	flagellar hook-ass
732	80.5	4.5	1349	2	S51471	killer toxin insen	805	78.5	4.3	556	2	A44441	B-cell antigen CD1
733	80.5	4.5	1375	2	JT0345	dextranucrase (EC	806	78.5	4.3	561	2	T45607	hypothetical prote
734	80.5	4.5	1433	2	T30261	chitinase (EC 3.2.	807	78.5	4.3	590	2	A56535	gadd34 protein - 1
735	80.5	4.5	1457	1	A48066	protein-tyrosine-p	808	78.5	4.3	592	2	S54489	phosphoribosylamin
736	80.5	4.5	1538	2	E70874	probable ppsB prot	809	78.5	4.3	605	1	A48665	methionyl-CoA
737	80.5	4.5	4588	2	T28667	dynein beta heavy	810	78.5	4.3	668	2	JQ0773	penicillin-binding
738	80	4.4	104	2	JH0345	T-cell receptor al	811	78.5	4.3	693	2	S46417	heat shock protein
739	80	4.4	150	2	A40862	fibroblast growth	812	78.5	4.3	759	2	B50520	ABC transporter at
740	80	4.4	233	2	I51383	Ig lambda chain -	813	78.5	4.3	759	2	AG3402	polyphosphate kina
741	80	4.4	239	2	G02630	FcalphaRb - human	814	78.5	4.3	829	2	E87305	TonB-dependent rec
742	80	4.4	287	2	JH0332	IGA (Fc) receptor,	815	78.5	4.3	934	2	B29838	parasporal crystal
743	80	4.4	313	2	T28598	hypothetical prote	816	78.5	4.3	1019	2	T40813	probable cell divi
744	80	4.4	425	2	JE0086	SH3-domain binding	817	78.5	4.3	1070	2	T34385	hypothetical prote
745	80	4.4	433	1	S48515	adenylosuccinate s	818	78.5	4.3	1217	2	T00270	hypothetical prote
746	80	4.4	454	1	MHYH	Ig mu chain C regi	819	78.5	4.3	1252	2	T31119	msHQ protein - Vib
747	80	4.4	466	2	H96991	secreted protein c	820	78.5	4.3	1385	2	A88554	protein C38C10.5a
748	80	4.4	552	2	S42253	probable N3L prote	821	78.5	4.3	1391	2	B88554	protein C38C10.5b
749	80	4.4	642	2	S44542	probable membrane	822	78.5	4.3	1440	2	JC6312	protein-tyrosine-p
750	80	4.4	680	2	PN0510	integrin beta-3 ch	823	78.5	4.3	1687	2	T43144	vitellogenin II pr
751	80	4.4	937	2	T04194	hypothetical prote	824	78.5	4.3	5188	2	B85547	probable RTX famli
752	80	4.4	995	2	A56599	embryo kinase 5 -	825	78.5	4.3	5291	2	F90696	hypothetical prote
753	80	4.4	1200	2	T48194	hypothetical prote	826	78	4.3	125	2	S62676	hegulin isoform
754	80	4.4	3343	2	T42207	breast cancer susc	827	78	4.3	131	2	PT0178	Ig kappa chain pre
755	79.5	4.4	155	2	A41675	telokin - rabbit	828	78	4.3	132	2	A55410	Ig light chain v r
756	79.5	4.4	204	2	A69197	hypothetical prote	829	78	4.3	137	2	C45893	T-cell receptor al
757	79.5	4.4	220	2	I55963	Lyt-2.1 lymphocyte	830	78	4.3	178	2	G71195	hypothetical prote
758	79.5	4.4	250	2	A34342	IGF Fc receptor al	831	78	4.3	233	2	S29577	Ig light chain - r
759	79.5	4.4	261	2	S29360	FC gamma (IgG) rec	832	78	4.3	255	2	JC7593	SH2 domain-contain

541	90	5.0	296	2	I46021	FC-gamma receptor	614	85	4.7	1526	2	T19473	hypothetical prote
542	90	5.0	432	1	RWCZT4	T-cell surface gly	615	85	4.7	2274	2	T30258	adenomatous polypo
543	90	5.0	444	2	G01924	KIR (cl-2) NK rece	616	85	4.7	2339	2	S41121	acetyl-CoA carboxy
544	90	5.0	576	2	A32604	interleukin-1 rece	617	85	4.7	4351	2	T00252	MEGF1 protein - ra
545	90	5.0	721	2	C82939	virulence associat	618	84.5	4.7	240	2	S01299	OX-45 membrane gly
546	90	5.0	858	1	VCLJG2	env polyprotein pr	619	84.5	4.7	243	2	A53244	leukocyte antigen
547	90	5.0	1357	2	T29265	hypothetical prote	620	84.5	4.7	330	2	A40071	FC-gamma-1/gamma-2
548	90	5.0	2282	2	T42717	DNA-binding protei	621	84.5	4.7	330	2	I49660	FC-gamma-1/gamma-2
549	89.5	5.0	131	2	F45893	T-cell receptor al	622	84.5	4.7	385	2	T01132	hypothetical prote
550	89.5	5.0	245	2	A30154	IGF receptor alpha	623	84.5	4.7	466	2	AF01172	asparagine-tRNA li
551	89.5	5.0	254	1	JU0107	FC gamma (IgG) rec	624	84.5	4.7	727	2	S45112	hypothetical prote
552	89.5	5.0	362	2	A56745	microfibril-associ	625	84.5	4.7	897	2	E65127	Probable bifunctio
553	89.5	5.0	1134	1	JN0711	protein-tyrosine k	626	84.5	4.7	1133	2	T01757	hypothetical prote
554	89.5	5.0	1691	1	D54689	protein-tyrosine-p	627	84.5	4.7	1227	2	T48028	hypothetical prote
555	89	4.9	257	2	PS0401	basigin type II -	628	84	4.7	136	1	KVMS21	Ig kappa chain pre
556	89	4.9	271	2	S43512	GP42/basigin prote	629	84	4.7	162	2	I51668	tumor suppressor -
557	89	4.9	273	2	JX0107	basigin precursor	630	84	4.7	225	2	G89936	conserved hypothet
558	89	4.9	275	2	PS0402	basigin type III -	631	84	4.7	240	2	JL0143	antigen BCM1.precu
559	89	4.9	429	1	EHRT	Ig epsilon chain C	632	84	4.7	246	2	A29523	T-cell surface gly
560	89	4.9	598	2	A57249	beta-galactosidase	633	84	4.7	337	2	AG0963	hypothetical prote
561	89	4.9	1452	1	S17669	secretory componen	634	84	4.7	466	2	JC5897	killer cell inhibi
562	89	4.9	331	2	T15587	protein-tyrosine-p	635	84	4.7	495	2	JC2195	vaoactive intesti
563	88.5	4.9	309	2	I49522	gene B7-2 protein	636	84	4.7	737	2	I39547	S-protein secretio
564	88	4.9	757	1	S48841	hypothetical prote	637	84	4.7	997	2	D75012	hypothetical prote
565	88	4.9	832	2	A1096	secretory componen	638	84	4.7	1442	2	S72441	protein-tyrosine-p
566	88	4.9	4336	2	E71086	internalin protein	639	84	4.7	1477	2	B43855	high-molecular-wei
567	88	4.9	151	2	T31607	hypothetical prote	640	84	4.7	1536	2	A43855	high-molecular-wei
568	87.5	4.8	280	2	I55577	hypothetical prote	641	83.5	4.6	110	2	B30583	I-cell receptor de
569	87.5	4.8	321	2	I54766	FC gamma (IgG) rec	642	83.5	4.6	134	2	S21917	Ig kappa chain V r
570	87.5	4.8	321	2	I54766	B-lymphocyte activ	643	83.5	4.6	245	2	T07071	beta-fructofuranos
571	87.5	4.8	368	2	S17980	pgal protein - Asp	644	83.5	4.6	315	1	HN24X	hemagglutinin prec
572	87.5	4.8	402	2	T29703	hypothetical prote	645	83.5	4.6	328	2	S30444	Sn2 protein - huma
573	87.5	4.8	660	2	H12376	probable tpr prote	646	83.5	4.6	374	2	S69339	Ig heavy chain V r
574	87	4.8	359	2	A97175	undecaprenyl-PP-Mu	647	83.5	4.6	405	1	B42606	cytochrome P450 CV
575	87	4.8	383	2	T21946	hypothetical prote	648	83.5	4.6	490	2	B96952	sucrase-6-phosphat
576	87	4.8	477	2	B41115	asparagine-tRNA li	649	83.5	4.6	513	2	F86320	hypothetical prote
577	87	4.8	814	2	I40048	S-layer protein pr	650	83.5	4.6	583	2	S57721	capB protein - Clo
578	87	4.8	974	1	A49714	protein-tyrosine k	651	83.5	4.6	1054	2	T18304	acid trehalase hom
579	87	4.8	2458	2	T17420	probable polyketid	652	83.5	4.6	1657	2	T25421	hypothetical prote
580	86.5	4.8	235	2	S25058	Ig kappa chain - m	653	83	4.6	220	2	A49444	Ig gamma-1 heavy c
581	86.5	4.8	278	1	TDRTOX	OX-2 membrane gly	654	83	4.6	313	2	JQ1862	3IR protein - vari
582	86.5	4.8	440	2	D71715	hypothetical prote	655	83	4.6	315	1	HN2VZV	hemagglutinin prec
583	86.5	4.8	1533	2	T00344	hypothetical prote	656	83	4.6	410	2	C69197	ATP-dependent 26S
584	86	4.8	387	2	T04320	polygalacturonase	657	83	4.6	555	2	JQ1526	interleukin-1 rece
585	86	4.8	387	2	T07591	polygalacturonase	658	83	4.6	563	2	C95874	conserved hypothet
586	86	4.8	444	2	G01925	KIR (cl-11) NK rec	659	83	4.6	633	2	AE2312	transketolase [imp
587	86	4.8	501	1	A60005	glycoprotein A pre	660	83	4.6	680	2	JC5895	killer cell inhibi
588	86	4.8	501	1	VBEMBA	glycoprotein A pre	661	83	4.6	767	2	S41479	DNA-binding protei
589	86	4.8	501	1	VBEMBA	glycoprotein A pre	662	83	4.6	1014	2	T24412	hypothetical prote
590	86	4.8	505	1	VBEMVH	glycoprotein gp57-	663	83	4.6	1033	2	A12359	hypothetical prote
591	86	4.8	580	2	A36683	hypothetical prote	664	83	4.6	2638	1	A42545	genome polypeptid
592	86	4.8	587	2	S36231	beta-fructofuranos	665	83	4.6	4836	2	T14346	herc2 protein - mo
593	86	4.8	856	1	A44963	env polyprotein pr	666	82.5	4.6	125	2	A53627	fibroblast growth
594	86	4.8	1394	2	S60762	IGA-specific serin	667	82.5	4.6	160	2	I47163	cytolytic trigger
595	86	4.8	1711	2	AB1283	peptidoglycan link	668	82.5	4.6	197	2	S29593	Ig kappa chain (WM
596	85.5	4.7	475	2	A54879	pregnancy-specific	669	82.5	4.6	233	2	JC5322	p53 specific singl
597	85.5	4.7	510	2	PC4054	cardiac C-protein	670	82.5	4.6	247	1	RWMS72	T-cell surface gly
598	85.5	4.7	593	1	DTCHPH	purH bifunctional	671	82.5	4.6	315	2	T37438	hemagglutinin - va
599	85.5	4.7	764	1	QRHUGS	secretory componen	672	82.5	4.6	429	2	T36088	probable secreted
600	85.5	4.7	1145	1	GNLJEW	HIV-1 retropepsin	673	82.5	4.6	433	2	S31436	Ig upsilon chain -
601	85.5	4.7	1146	1	GNLJ22	HIV-1 retropepsin	674	82.5	4.6	610	2	T25262	hypothetical prote
602	85.5	4.7	1146	1	GNLJEW	HIV-1 retropepsin	675	82.5	4.6	871	2	H81430	translation initia
603	85.5	4.7	1732	2	T30836	lysine-specific cy	676	82.5	4.6	1553	2	T18502	hypothetical prote
604	85	4.7	505	2	B84831	hypothetical prote	677	82	4.5	120	2	D29775	Ig kappa chain pre
605	85	4.7	635	2	JC5896	killer cell inhibi	678	82	4.5	225	2	I51335	Ig lambda chain -
606	85	4.7	753	2	B36268	platelet glycoprot	679	82	4.5	230	2	S49449	FC-gamma receptor
607	85	4.7	778	2	A60798	platelet glycoprot	680	82	4.5	270	2	A34636	B-cell-restrict
608	85	4.7	788	2	I77349	platelet glycoprot	681	82	4.5	280	2	A45803	hemagglutinin - va
609	85	4.7	788	2	A26547	platelet glycoprot	682	82	4.5	313	2	H36854	K9R protein - vari
610	85	4.7	817	2	A48721	titin, muscle - ch	683	82	4.5	318	2	F72171	glycoprotein A - t
611	85	4.7	832	2	E71492	hypothetical prote	684	82	4.5	489	1	VBETA	glycoprotein gp57-
612	85	4.7	939	2	I41197	eeae protein (enter	685	82	4.5	523	1	A60408	hypothetical prote
613	85	4.7	1436	2	JC5290	protein-tyrosine-p	686	82	4.5	630	2	T38637	

395	113.5	6.3	374	1	A39878	Fc gamma (IgG) rec	468	100	5.5	395	2	T05906	probable polygalact
396	113.5	6.3	547	1	S28904	intercellular adhe	469	100	5.5	531	2	S06016	intercellular adhe
397	113.5	6.3	1465	1	S43529	165K protein, skel	470	100	5.5	537	2	I49769	intercellular adhe
398	113	6.3	530	2	A53437	poliovirus recepto	471	100	5.5	641	2	D71170	hypothetical prote
399	112.5	6.2	304	1	RMCHH7	cell surface glyco	472	99	5.5	537	2	A45815	intercellular adhe
400	112.5	6.2	503	2	JC5287	SHP substrate-1 pr	473	99	5.5	869	2	T44440	chitinase (EC 3.2.
401	112.5	6.2	666	2	H99581	protein dim-1 (imp	474	99	5.5	1160	2	F88369	protein unc-52 (im
402	112.5	6.2	954	2	I51703	c-kit-related kina	475	98.5	5.5	629	2	A46500	Ly-9.2 antigen - m
403	112.5	6.2	2109	2	E89066	protein H05009.1 (476	98	5.4	238	2	A49633	Ig lambda-like cha
404	112.5	6.2	2109	2	T33247	hypothetical prote	477	98	5.4	524	2	JQ0683	type-specific anti
405	112	6.2	512838	precu	Ig mu chain precu	478	98	5.4	544	2	JC5018	intercellular adhe	
406	112	6.2	1327	2	T09402	immunoglobulin-lik	479	98	5.4	773	1	QRRBG	secretory componen
407	111.5	6.2	335	2	CS4312	pregnancy-specific	480	98	5.4	1000	2	I46521	titin - rabbit (fr
408	111.5	6.2	392	2	B44194	poliovirus recepto	481	97.5	5.4	197	2	PQ0327	heparin-binding fi
409	111.5	6.2	417	2	A44194	poliovirus recepto	482	97.5	5.4	270	2	S65739	basigin precursor
410	111.5	6.2	567	2	S29498	lymphocyte antigen	483	97	5.4	172	2	B26414	95K nonspecific cr
411	111	6.1	210	2	JC4122	pregnancy-specific	484	97	5.4	465	2	B97235	deacetylase/di pep
412	111	6.1	292	2	T44230	hypothetical prote	485	97	5.4	874	2	T29548	hypothetical prote
413	111	6.1	398	2	S17428	interleukin-1 rece	486	96.5	5.3	309	2	I49503	B-lymphocyte activ
414	111	6.1	748	2	S41050	fibroblast growth	487	96.5	5.3	364	2	T46926	hypothetical prote
415	110.5	6.1	509	2	JC5288	SHP substrate-1 pr	488	96.5	5.3	437	2	A64488	hypothetical prote
416	110.5	6.1	513	2	JC5289	SHP substrate-1 pr	489	96.5	5.3	475	2	I76668	pregnancy-specific
417	110	6.1	285	2	S36903	Fc gamma (IgG) rec	490	96.5	5.3	580	2	A46538	Ig heavy chain, se
418	110	6.1	508	2	A33378	fasciclin III prec	491	96.5	5.3	709	2	A35364	carcinoembryonic a
419	110	6.1	919	2	T32541	unc-5 protein - Ca	492	96	5.3	455	1	MEHMS	Ig mu chain C regi
420	110	6.1	1579	2	B91290	probable invasin (493	96	5.3	455	2	A24976	Ig mu chain C regi
421	110	6.1	1700	2	G86131	hypothetical prote	494	96	5.3	476	1	MEHSM	Ig mu chain C regi
422	109.5	6.1	164	2	T19795	hypothetical prote	495	96	5.3	562	2	G02426	interleukin-1 rece
423	109.5	6.1	196	2	T19794	hypothetical prote	496	96	5.3	790	1	TVHUTT	nerve growth facto
424	109.5	6.1	206	2	A40305	biliary glycoprote	497	95.5	5.3	309	2	S15674	cell surface glyco
425	109.5	6.1	470	2	S22080	Ig heavy chain pre	498	95.5	5.3	330	2	A29915	teratocarcinoma gl
426	109.5	6.1	532	1	A29849	intercellular adhe	499	95.5	5.3	345	2	A46052	vascular cell adhe
427	108	6.0	207	2	A56190	titin - rat (fragm	500	95.5	5.3	375	2	I60125	PDGF receptor beta
428	108	6.0	267	2	I72882	Fc gamma receptor	501	95	5.3	267	2	A35902	Fc gamma (IgG) rec
429	108	6.0	467	1	HLMSP3	poliovirus recepto	502	95	5.3	277	2	I52825	gene MAC25 protein
430	108	6.0	474	1	OMHU1B	alpha-1-B-glycopro	503	95	5.3	282	2	S50031	prostatic-stimu
431	107.5	6.0	352	2	I77374	pregnancy-specific	504	95	5.3	329	2	A44065	fibroblast growth
432	107.5	6.0	404	2	A46480	Fc gamma (IgG) rec	505	95	5.3	799	1	TVRTTB	nerve growth facto
433	107.5	6.0	537	2	A46611	myosin-binding pro	506	95	5.3	3283	2	AC1018	large repetitive p
434	106.5	5.9	336	2	S42632	fit-1S protein pre	507	94.5	5.2	182	2	A34647	pregnancy-specific
435	106.5	5.9	367	1	MHCH	Ig mu chain C regi	508	94.5	5.2	355	2	D72174	D9R protein - vari
436	106	5.9	407	2	T08732	hypothetical prote	509	94.5	5.2	1184	2	T09484	cartilage intermed
437	105.5	5.8	326	2	T37450	interleukin-1 beta	510	94.5	5.2	1280	2	AB1981	hypothetical prote
438	105.5	5.8	487	2	T28804	hypothetical prote	511	94.5	5.2	1452	1	S17670	protein-tyrosine-p
439	105	5.8	131	2	T20334	hypothetical prote	512	94.5	5.2	2347	1	TVHURS	kinase-related pro
440	105	5.8	269	2	A46506	leukocyte activati	513	94	5.2	328	2	I47159	Ig gamma 2a chain
441	104.5	5.8	290	2	F42527	B16R protein - vac	514	94	5.2	757	2	I45956	polymeric immunogl
442	104	5.8	1471	2	T19506	hypothetical prote	515	93.5	5.2	194	2	T29925	hypothetical prote
443	103.5	5.7	240	2	JC4121	pregnancy-specific	516	93.5	5.2	265	2	A55811	carcinoembryonic a
444	103.5	5.7	326	1	WMVZ15	B15R protein precu	517	93.5	5.2	354	2	S46877	B20R protein - var
445	103.5	5.7	487	2	S65133	butyrophilin - mou	518	93.5	5.2	354	2	T28616	hypothetical prote
446	103.5	5.7	531	2	S20900	titin - mouse (fra	519	93.5	5.2	1366	2	B84924	hypothetical prote
447	103.5	5.7	538	2	I68093	PRR2 delta - human	520	93	5.1	144	2	B40098	colorectal cancer
448	103	5.7	618	2	T08685	hypothetical prote	521	93	5.1	267	2	I56110	Fc-gamma RIIb-alp
449	103	5.7	943	2	B45082	neurotrophic recep	522	93	5.1	299	2	I46690	CD80 precursor - r
450	102.5	5.7	257	2	S00682	IgE Fc receptor al	523	93	5.1	352	2	T33433	hypothetical prote
451	102.5	5.7	336	2	I48471	Fc gamma (IgG) rec	524	93	5.1	293	2	S16844	titin - rabbit (fr
452	102.5	5.7	1021	2	I39207	leukocyte surface	525	92.5	5.1	213	2	JE0247	Ig lambda chain NI
453	102	5.6	351	1	SAVZVV	surface antigen pr	526	92.5	5.1	274	2	T32736	hypothetical prote
454	102	5.6	478	2	I53960	PRR2 alpha - human	527	92.5	5.1	298	2	H64247	translation elonga
455	102	5.6	1398	2	T25568	hypothetical prote	528	92.5	5.1	590	2	I56526	interleukin 1 rece
456	101.5	5.6	275	2	JC7604	CD86 spliced varia	529	92.5	5.1	1220	2	T32916	hypothetical prote
457	101.5	5.6	329	1	A48754	B7-2 antigen - hum	530	92	5.1	328	2	I47160	Ig gamma 2b chain
458	101.5	5.6	625	2	T16777	hypothetical prote	531	92	5.1	460	2	JC02194	vasoactive intestei
459	101.5	5.6	937	2	A45082	neurotrophic recep	532	92	5.1	545	2	JU0341	intercellular adhe
460	101	5.6	351	1	SAVZWR	surface antigen pr	533	91.5	5.1	455	2	H96797	hypothetical prote
461	101	5.6	353	1	SAVZVC	surface antigen pr	534	91	5.0	132	2	S14077	Ig kappa chain - A
462	101	5.6	421	2	T46266	hypothetical prote	535	91	5.0	370	2	A96741	hypothetical prote
463	101	5.6	458	1	RWHUT4	T-cell surface gly	536	91	5.0	416	2	S33473	interleukin-1 rece
464	101	5.6	751	2	I48748	semaphorin E - mou	537	91	5.0	427	2	G02034	killer cell inhibi
465	100.5	5.6	274	2	A47639	OX-2 membrane glyc	538	90.5	5.0	391	2	T09058	butyrophilin homol
466	100	5.5	235	2	S20000	Ig light chain pre	539	90.5	5.0	1269	2	F90538	hypothetical prote
467	100	5.5	304	2	B88746	protein C18F3.3 (i	540	90	5.0	283	1	FCMSG1	Fc gamma (IgG) rec

249 137 7.6 282 2 C28928 pregnancy-specific
 250 137 7.6 424 2 B36109 pregnancy-specific
 251 137 7.6 458 2 S68177 C-CAM2a protein is
 252 137 7.6 519 2 A44783 ecto-ATPase precu
 253 137 7.6 524 2 S35341 ketin - fruit fly
 254 136.5 7.6 738 2 A40096 platelet-endotheli
 255 136.5 7.6 822 2 S19947 fibroblast growth
 256 136.5 7.5 822 2 B49151 fibroblast growth
 257 135.5 7.5 975 2 T30816 macrophage colony-
 258 134.5 7.4 419 2 J42123 pregnancy-specific
 259 134.5 7.4 428 2 S17486 pregnancy-specific
 260 134.5 7.4 428 2 J50032 pregnancy-specific
 261 134.5 7.4 480 2 A56182 fibroblast growth
 262 134.5 7.4 627 2 B41288 vascular cell adhe
 263 134.5 7.4 729 2 A49120 fibroblast growth
 264 134 7.4 238 2 T22098 hypothetical prote
 265 134 7.4 424 2 A34595 pregnancy-specific
 266 134 7.4 1147 2 A59307 myosin-light-chain
 267 133.5 7.4 888 2 S23065 ufo protein - mous
 268 133 7.4 336 2 C32658 pregnancy-specific
 269 133 7.4 413 2 A37778 hemolin precursor
 270 133 7.4 473 2 D88976 protein F54E2.4 [i
 271 133 7.4 612 2 I73633 gene trkC protein
 272 133 7.4 818 2 A45058 fibroblast growth
 273 133 7.4 825 2 A55178 neurotrophin recep
 274 133 7.4 839 1 I73632 neurotrophin-3 rec
 275 132.5 7.3 273 2 B28928 pregnancy-specific
 276 132.5 7.3 275 2 A28928 pregnancy-specific
 277 132.5 7.3 584 2 I50419 s-glycerin precurs
 278 132.5 7.3 856 2 I58411 protein-tyrosine k
 279 132 7.3 1048 2 T30815 platelet-derived g
 280 131.5 7.3 480 2 B56182 fibroblast growth
 281 131.5 7.3 707 2 A38429 keratinocyte growt
 282 131 7.3 899 2 S33766 platelet-derived g
 283 131 7.3 811 2 P06089 connectin 1 - chic
 284 131 7.3 1106 1 PFHUGB platelet-derived g
 285 130.5 7.2 310 2 J10119 Fc gamma (IgG) rec
 286 130.5 7.2 323 2 S06946 Fc gamma (IgG) rec
 287 130 7.2 802 1 TVHUF4 fibroblast growth
 288 129.5 7.2 419 2 A36109 pregnancy-specific
 289 129.5 7.2 707 2 A54846 fibroblast growth
 290 129.5 7.2 1040 2 A57638 receptor tyrosine
 291 129.5 7.2 1103 2 T22889 hypothetical prote
 292 129 7.1 392 1 RWHUPD poliovirus recepto
 293 129 7.1 417 1 RWHUPA poliovirus recepto
 294 129 7.1 1098 1 PFM5RB platelet-derived g
 295 128.5 7.1 682 2 A35969 heparin-binding gr
 296 128 7.1 806 1 TVHUF3 fibroblast growth
 297 127.5 7.1 241 2 S32359 glial growth facto
 298 127 7.0 992 2 A39311 protein-tyrosine k
 299 126.5 7.0 592 2 S25705 Ig mu chain - shee
 300 126.5 7.0 790 2 A39627 protein-tyrosine k
 301 126 7.0 477 1 I73631 brain-derived neur
 302 126 7.0 822 1 A56853 brain-derived neur
 303 126 7.0 940 2 A40985 projectin - fruit
 304 126 7.0 1000 2 S18827 Flt3 protein - mou
 305 125.5 6.9 251 2 T15495 hypothetical prote
 306 125.5 6.9 278 2 J15007 biliary glycoprote
 307 125.5 6.9 335 2 B33251 nonspecific cross-
 308 125.5 6.9 341 2 J15111 biliary glycoprote
 309 125.5 6.9 518 2 J4024 poliovirus recepto
 310 125.5 6.9 526 2 S70587 butyrophilin precu
 311 125.5 6.9 975 1 TVMSKT protein-tyrosine k
 312 125 6.9 278 2 J1506 biliary glycoprote
 313 125 6.9 341 2 J1512 biliary glycoprote
 314 125 6.9 977 2 I45877 protein-tyrosine k
 315 124.5 6.9 750 2 S41051 fibroblast growth
 316 124.5 6.9 829 2 J40583 fibroblast growth
 317 124.5 6.9 960 1 JN0677 protein-tyrosine k
 318 124 6.9 278 2 A39037 carcinoembryonic a
 319 124 6.9 426 2 C55181 pregnancy-specific
 320 124 6.9 426 2 S09016 pregnancy-specific
 321 124 6.9 426 2 B35334 pregnancy-specific

322 124 6.9 436 2 B55181 pregnancy-specific
 323 124 6.9 495 2 A55181 pregnancy-specific
 324 124 6.9 650 1 J1450 fibroblast growth
 325 124 6.9 999 2 J38547 novel cellular pro
 326 124 6.9 1666 2 A48594 skelemin - mouse
 327 123.5 6.8 402 2 A54312 pregnancy-specific
 328 123.5 6.8 640 2 A43273 heregulin precurs
 329 123 6.8 351 2 B34595 pregnancy-specific
 330 123 6.8 476 1 A35104 brain-derived neur
 331 123 6.8 821 1 S06943 brain-derived neur
 332 123 6.8 1176 2 JN0583 myosin-light-chain
 333 122.5 6.8 230 2 A56210 heregulin precurs
 334 122.5 6.8 241 2 D43273 heregulin precurs
 335 122.5 6.8 462 2 I38404 neu differentiatio
 336 122.5 6.8 636 2 I61718 neu differentiatio
 337 122.5 6.8 637 2 C43273 heregulin precurs
 338 122.5 6.8 639 2 I61719 heregulin, splice
 339 122.5 6.8 645 2 B43273 heregulin, splice
 340 122.5 6.8 662 2 I61722 neu differentiatio
 341 122 6.8 272 2 I48268 biliary glycoprote
 342 122 6.8 850 2 J05700 ErbB kinase activa
 343 121.5 6.7 332 2 JN0067 pregnancy-specific
 344 121.5 6.7 365 2 J07780 coxsackie- and ade
 345 121.5 6.7 474 1 C39667 brain-derived neur
 346 121.5 6.7 476 1 B39667 brain-derived neur
 347 121.5 6.7 520 1 S44099 brain-derived neur
 348 121.5 6.7 818 1 S44098 brain-derived neur
 349 121.5 6.7 821 1 A39667 brain-derived neur
 350 121.5 6.7 1450 2 A44027 165K myofibrillar
 351 121 6.7 292 2 T44044 glycoprotein [impo
 352 121 6.7 733 2 I49293 fibroblast growth
 353 121 6.7 994 2 I49276 c-met tyrosine kin
 354 121 6.7 1142 2 S36845 myosin-binding pro
 355 120.5 6.7 212 2 C33258 pregnancy-specific
 356 120.5 6.7 353 2 S51242 heparin-binding fi
 357 120.5 6.7 1742 2 S24600 projectin - fruit
 358 120 6.6 729 2 A56795 fibroblast growth
 359 119.5 6.6 684 2 S60266 novel antigen rece
 360 119.5 6.6 6805 2 S20901 titin - rabbit (fr
 361 119 6.6 707 2 J07763 neuronal leucine-r
 362 119 6.6 820 2 S17295 fibroblast growth
 363 119 6.6 860 2 J05702 ErbB kinase activa
 364 119 6.6 868 2 J05701 ErbB kinase activa
 365 119 6.6 888 2 S55050 cardiac myosin-bin
 366 118 6.5 1451 2 S42167 190K protein - hum
 367 117.5 6.5 182 2 I83053 pregnancy-specific
 368 117.5 6.5 335 2 A33514 pregnancy-specific
 369 117.5 6.5 569 2 A36187 interleukin-1 rece
 370 117.5 6.5 978 1 A49814 protein-tyrosine k
 371 117 6.5 621 2 B57431 myosin-binding C-p
 372 117 6.5 825 1 A40026 neurotrophin-3 rec
 373 117 6.5 894 1 A41527 protein-tyrosine k
 374 116.5 6.5 243 2 A37982 calcium vector pro
 375 116.5 6.5 282 2 T17219 hypothetical prote
 376 116.5 6.5 317 2 J10118 Fc gamma (IgG) rec
 377 116.5 6.5 599 2 T16774 hypothetical prote
 378 116 6.4 253 2 T15475 hypothetical prote
 379 116 6.4 268 2 T23555 hypothetical prote
 380 116 6.4 330 2 I46691 CD86 precursor - r
 381 116 6.4 416 2 A54017 colon carcinoma-as
 382 116 6.4 993 2 A36873 protein-tyrosine k
 383 115.5 6.4 526 2 A37821 butyrophilin - bov
 384 115.5 6.4 942 2 S23251 protein-tyrosine k
 385 115 6.4 166 2 A33402 pregnancy-specific
 386 115 6.4 813 1 A49123 fibroblast growth
 387 115 6.4 1462 1 B36182 protein-tyrosine-p
 388 114.5 6.3 326 2 J04124 pregnancy-specific
 389 114 6.3 302 2 C36454 fibroblast growth
 390 114 6.3 432 1 RWMQ14 T-cell surface gly
 391 114 6.3 713 2 I50128 fibroblast growth
 392 114 6.3 947 1 B44294 unc-5 protein, lon
 393 114 6.3 1132 2 A35089 myosin-binding pro
 394 113.5 6.3 344 2 A41357 Fc gamma (IgG) rec

103	173.5	9.6	1021	2	T42634	connectin/titin -	176	151	8.4	976	1	TWMSMD	macrophage colony-
104	172.5	9.6	264	2	T26976	hypothetical prote	177	151	8.4	1287	2	T30988	hypothetical prote
105	172.5	9.6	264	2	T29583	hypothetical prote	178	150.5	8.3	349	2	A34815	carcinoembryonic a
106	172.5	9.6	1880	2	T18531	tractin - medicina	179	150.5	8.3	824	2	S24108	protein-tyrosine k
107	172	9.5	286	2	A28333	carcinoembryonic a	180	150.5	8.3	1298	2	A48999	protein-tyrosine k
108	172	9.5	647	2	A35648	B-cell adhesion pr	181	150	8.3	769	2	S16236	fibroblast growth
109	171.5	9.5	1338	2	S09982	protein-tyrosine k	182	150	8.3	822	2	A45081	fibroblast growth
110	171	9.5	464	2	C30127	transmembrane carc	183	150	8.3	822	2	A41794	keratinocyte growt
111	171	9.5	526	1	A32164	biliary glycoprote	184	149.5	8.3	739	2	J50675	protein-tyrosine-p
112	171	9.5	1257	1	A41060	neural cell adhe	185	149.5	8.3	1501	2	I58148	vascular cell adhe
113	170	9.4	812	1	A36477	fibroblast growth	186	149.5	8.3	1863	2	S46217	protein-tyrosine-p
114	169	9.4	764	2	A34448	irregular chiasm C	187	149	8.3	335	2	H43354	pregnancy-specific
115	169	9.4	814	1	A39752	fibroblast growth	188	149	8.3	1894	2	C34689	protein-tyrosine-p
116	168	9.3	1330	2	S49018	embryonic receptor	189	148.5	8.2	587	2	JH0464	DM-GRASP precursor
117	168	9.3	2051	2	T30938	receptor tyrosine	190	148.5	8.2	588	2	JH0506	adhesion molecule
118	168	9.3	2295	2	C88369	protein unc-52 (im	191	148.5	8.2	1907	2	S50893	protein-tyrosine-p
119	167.5	9.3	523	2	I50478	neurolin - goldfis	192	147.5	8.2	876	2	I49152	protein-tyrosine k
120	167.5	9.3	1694	2	S50065	sialoadhesin - mou	193	147.5	8.2	1499	2	I50212	protein-tyrosine-p
121	167	9.2	816	2	A49151	fibroblast growth	194	147	8.1	402	2	T09062	probable advanced
122	167	9.2	822	1	TWMSFG	fibroblast growth	195	147	8.1	406	2	E43354	pregnancy-specific
123	167	9.2	1356	2	JC1402	protein-tyrosine k	196	146.5	8.1	773	2	T46283	hypothetical prote
124	165.5	9.2	538	2	JC2457	vascular cell adhe	197	146	8.1	428	2	A27658	pregnancy-specific
125	165.5	9.2	646	2	I38049	cell surface glyco	198	146	8.1	852	2	I51259	tyrosine kinase C
126	165	9.1	584	2	T08678	hypothetical prote	199	146	8.1	1088	1	PRKTA	platelet-derived g
127	165	9.1	822	2	I49289	fibroblast growth	200	146	8.1	1089	1	S33727	platelet-derived g
128	165	9.1	822	2	S29840	fibroblast growth	201	145.5	8.1	739	2	JN0581	vascular cell adhe
129	165	9.1	2222	2	T13924	sdh protein - frui	202	145.5	8.1	799	2	S18209	fibroblast growth
130	164.5	9.1	583	2	I39428	alcam - human	203	145.5	8.1	1898	2	S46216	leukocyte antigen-
131	164.5	9.1	832	2	JH0393	fibroblast growth	204	145	8.0	972	1	TWUMD	macrophage colony-
132	164	9.1	628	2	I38000	lutheran blood gro	205	144.5	8.0	1262	1	B48758	protein-tyrosine-p
133	163	9.0	818	2	T19120	hypothetical prote	206	144.5	8.0	1496	1	A48758	protein-tyrosine-p
134	162.5	9.0	1535	2	S46224	peroxidasin - frui	207	143.5	7.9	1177	2	T16594	hypothetical prote
135	162	9.0	321	2	JH0395	biliary glycoprote	208	143.5	7.9	13055	2	T16580	hypothetical prote
136	162	9.0	351	2	JH0396	biliary glycoprote	209	143	7.9	620	2	JH0593	Schwann cell myeli
137	162	9.0	417	2	JH0394	biliary glycoprote	210	143	7.9	687	2	A49636	soluble vascular e
138	161	8.9	588	2	I37202	B-CAM protein - hu	211	143	7.9	1011	2	T13669	neuromusculin - fr
139	161	8.9	2541	2	T29340	hypothetical prote	212	142.5	7.9	326	2	F43354	pregnancy-specific
140	160.5	8.9	980	1	TVCTMD	macrophage colony-	213	142.5	7.9	435	2	D33258	pregnancy-specific
141	160	8.9	662	2	C40862	heparin-binding gr	214	142.5	7.9	739	2	A41288	vascular cell adhe
142	160	8.9	822	1	TVHUF8	fibroblast growth	215	142	7.9	806	2	A35963	protein-tyrosine k
143	160	8.9	1437	2	T31093	probable protein-t	216	141.5	7.8	324	2	G43354	pregnancy-specific
144	160	8.9	6831	2	A88552	protein unc-22 (im	217	141.5	7.8	333	2	A43354	pregnancy-specific
145	160	8.9	6839	2	S57242	twitchin (similar	218	141.5	7.8	789	2	T28714	hypothetical prote
146	158.5	8.8	1199	2	T23005	hypothetical prote	219	141.5	7.8	1227	2	T23004	hypothetical prote
147	158	8.7	361	2	PN0020	fibroblast growth	220	141.5	7.8	1355	2	T28715	hypothetical prote
148	158	8.7	822	2	B54846	fibroblast growth	221	141	7.8	254	2	C42691	fibroblast growth
149	157.5	8.7	941	1	TWVMD	protein-tyrosine k	222	141	7.8	821	1	TVHUF2	fibroblast growth
150	157	8.7	299	2	S56749	functional adhesio	223	140.5	7.8	397	2	C43354	pregnancy-specific
151	156.5	8.7	416	1	A42879	advanced glycosyla	224	140.5	7.8	705	2	S51635	fibroblast growth
152	156	8.6	978	2	S16385	macrophage colony-	225	140.5	7.8	823	2	B35963	protein-tyrosine k
153	156	8.6	7160	2	T27935	hypothetical prote	226	140.5	7.8	1089	1	PFHUGA	platelet-derived g
154	155.5	8.6	880	2	B53743	protein-tyrosine k	227	140	7.8	800	1	TVHUF2	fibroblast growth
155	155.5	8.6	1138	2	S24614	myosin-binding pro	228	140	7.8	800	2	A48991	heparin-binding gr
156	155	8.6	458	1	MMWSR1	biliary glycoprote	229	140	7.8	801	2	I55363	fibroblast growth
157	155	8.6	458	2	JC1509	biliary glycoprote	230	140	7.8	890	1	A53743	protein-tyrosine k
158	155	8.6	521	2	JC1508	biliary glycoprote	231	140	7.8	976	1	TVHUKT	protein-tyrosine k
159	155	8.6	521	2	S34338	biliary glycoprote	232	139.5	7.7	395	2	D43354	pregnancy-specific
160	155	8.6	1363	2	I58375	protein-tyrosine k	233	139.5	7.7	417	2	A32877	pregnancy-specific
161	155	8.6	1367	2	A41228	protein-tyrosine k	234	139.5	7.7	419	2	A33258	pregnancy-specific
162	154.5	8.6	602	2	A45769	acetylcholine rece	235	139.5	7.7	419	2	A31135	pregnancy-specific
163	154.5	8.6	1897	1	TDHULK	leukocyte antigen-	236	139.5	7.7	426	2	A35964	pregnancy-specific
164	154	8.5	1348	2	S51656	vascular endotheli	237	139.5	7.7	821	1	TWMSBK	fibroblast growth
165	153.5	8.5	588	2	A45254	surface glycoprote	238	139.5	7.7	1052	2	B49120	protein-tyrosine k
166	153	8.5	1312	2	A56178	protein-tyrosine-p	239	139	7.7	824	2	S36439	fibroblast growth
167	152.5	8.4	267	2	A38442	probable tumor sup	240	139	7.7	987	2	A88746	protein C18F3.2 [i
168	152.5	8.4	458	2	S23969	cell-adhesion mole	241	139	7.7	3488	2	T34418	hypothetical prote
169	152	8.4	525	1	A58674	neurotrophin-3 rec	242	138.5	7.7	413	2	S65948	hemolin - cecropia
170	152	8.4	803	1	S35695	neurotrophin-3 rec	243	138.5	7.7	426	2	B33258	pregnancy-specific
171	152	8.4	819	1	TVCHFG	fibroblast growth	244	138.5	7.7	426	2	A35341	pregnancy-specific
172	152	8.4	880	1	JC4166	protein-tyrosine k	245	138	7.6	1087	2	I51552	platelet-derived g
173	152	8.4	123	2	S36846	myosin-binding pro	246	137.5	7.6	419	2	B54312	pregnancy-specific
174	151.5	8.4	344	2	A27681	nonspecific cross-	247	137.5	7.6	882	2	I38912	receptor tyrosine
175	151.5	8.4	422	2	S32357	glial growth facto	248	137.5	7.6	1379	2	JC4954	vascular endotheli

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OM protein - protein search, using sw model

Run on: June 3, 2005, 14:22:01 ; Search time 25 Seconds
(without alignments)
1323.943 Million cell updates/sec

Title: US-09-978-544A-523
Perfect score: 1806
Sequence: 1 MKTIQPKWHSISWAIFGL.....RRAGCVWLLPLLVLHLLKF 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : PIR_79:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1268	70.2	345	2	JC4025
4	1266	70.1	345	2	S03199
5	1259	69.7	345	2	JC1239
6	936.5	51.9	338	2	JC5519
7	931.5	51.6	338	2	JC4776
8	297.5	16.5	333	2	A31923
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10	283.5	15.7	1115	1	IJMSNL
11	279.5	15.5	725	2	J50099
12	279.5	15.5	1091	1	IJCHNL
13	278.5	15.4	4162	2	T42633
14	277.5	15.4	858	1	IJRTNC
15	277.5	15.4	1088	1	IJXLNL
16	276	15.3	761	1	IJHUNG
17	275.5	15.3	853	1	IJBONC
18	273.5	15.1	725	2	J50100
19	272.5	15.1	1323	2	PN0568
20	270.5	15.0	1092	1	JN0635
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22	259	14.3	7962	2	I38346
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837.422 Million cell updates/sec

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Post-processing: Minimum Match 0%
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES					
Result	Score	Query Match	Length	ID	Description

51	1806	100.0	344	14	US-10-066-269-104
53	1806	100.0	344	14	US-10-167-749-523
61	1806	100.0	344	14	US-10-223-085-56
225	1806	100.0	344	14	US-10-223-085-56
231	1806	100.0	344	14	US-10-219-065-126
261	1806	100.0	344	14	US-10-223-084-56
262	1806	100.0	344	14	US-10-223-088-56
263	1806	100.0	344	14	US-10-223-090-56
268	1806	100.0	344	14	US-10-223-087-56
270	1806	100.0	344	14	US-10-223-083-56
273	1806	100.0	344	14	US-10-223-089-56
446	1806	100.0	344	14	US-10-223-081-56
484	1806	100.0	344	14	US-10-223-082-56
553	1806	100.0	344	15	US-10-170-481A-523
555	1806	100.0	344	15	US-10-210-028-523

51	1806	100.0	344	14	US-10-066-269-104
53	1806	100.0	344	14	US-10-167-749-523
61	1806	100.0	344	14	US-10-223-085-56
225	1806	100.0	344	14	US-10-223-085-56
231	1806	100.0	344	14	US-10-219-065-126
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262	1806	100.0	344	14	US-10-223-088-56
263	1806	100.0	344	14	US-10-223-090-56
268	1806	100.0	344	14	US-10-223-087-56
270	1806	100.0	344	14	US-10-223-083-56
273	1806	100.0	344	14	US-10-223-089-56
446	1806	100.0	344	14	US-10-223-081-56
484	1806	100.0	344	14	US-10-223-082-56
553	1806	100.0	344	15	US-10-170-481A-523
555	1806	100.0	344	15	US-10-210-028-523

614	1806	100.0	344	15	US-10-162-521A-523
622	1806	100.0	344	15	US-10-305-654-56
634	1806	100.0	344	15	US-10-657-103-3
638	1806	100.0	344	15	US-10-081-056-56
646	1806	100.0	344	17	US-10-918-851-523
647	1806	100.0	344	17	US-10-931-886-376
648	1806	100.0	344	17	US-10-805-667-523
649	1806	100.0	344	17	US-10-897-359-523
651	1806	100.0	344	17	US-10-893-802-523
652	1806	100.0	344	17	US-10-897-360-523
653	1799	99.6	344	9	US-09-966-546-4
654	1799	99.6	344	9	US-09-966-546-6
655	1799	99.6	344	9	US-09-966-545-4
656	1799	99.6	344	9	US-09-966-545-6
657	1799	99.6	344	10	US-09-965-212-4
658	1799	99.6	344	10	US-09-965-212-6
659	1799	99.6	344	14	US-10-189-940-4
660	1799	99.6	344	14	US-10-189-940-6
661	1665.5	92.2	344	14	US-10-161-572-50
662	1665.5	92.2	344	15	US-10-295-027-456
663	1650	91.4	355	14	US-10-306-133-1
664	1642	90.9	313	15	US-10-557-103-4
665	1639.5	90.8	313	15	US-10-306-133-3
666	1427.5	79.0	344	15	US-10-015-115-87
667	1295	71.7	250	16	US-10-311-823-15
668	1285.5	71.2	338	15	US-10-015-115-86
669	1268	70.2	345	14	US-10-161-572-59
670	1268	70.2	345	15	US-10-015-115-84
671	1266	70.1	345	17	US-10-696-639-46
672	1266	70.1	345	15	US-10-015-115-83
673	1259	69.7	338	15	US-10-015-115-85
674	938.5	52.0	338	15	US-10-038-854-159
675	931.5	51.6	338	9	US-09-808-602-69
676	931.5	51.6	338	10	US-09-800-198-58
677	931.5	51.6	338	14	US-10-161-572-58
678	931.5	51.6	338	15	US-10-038-854-158
679	931.5	51.6	338	15	US-10-042-865-92
680	930.5	51.5	350	9	US-09-808-602-71
681	930.5	51.5	350	10	US-09-800-198-60
682	926.5	51.3	338	9	US-09-808-602-72
683	926.5	51.3	338	10	US-09-800-198-61
684	926.5	51.3	338	15	US-10-042-865-91
685	893	49.4	383	10	US-09-978-418-38
686	873.5	48.4	203	15	US-10-187-975-108
687	852.5	47.2	326	14	US-10-106-698-5794
688	842	46.6	352	15	US-10-038-854-156
689	842	46.6	352	15	US-10-042-865-89
696	823	45.6	354	14	US-10-066-269-130
744	823	45.6	354	14	US-10-219-065-2
800	823	45.6	354	15	US-10-038-854-24
803	823	45.6	354	15	US-10-312-352-15
805	822	45.5	354	15	US-10-042-865-14
806	820	45.4	354	15	US-10-104-047-2965
807	819	45.3	354	15	US-10-038-854-26
808	815	45.1	348	14	US-10-161-572-56
809	815	45.1	348	14	US-10-161-572-57
810	815	45.1	348	15	US-10-038-854-155
811	815	45.1	348	15	US-10-042-865-88
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881	815	45.1	352	15	US-10-170-481A-612
883	815	45.1	352	15	US-10-210-028-612
888	815	45.1	352	15	US-10-162-521A-612
899	815	45.1	352	17	US-10-918-851-612
900	815	45.1	352	17	US-10-805-667-612
901	815	45.1	352	17	US-10-897-359-612
902	815	45.1	352	17	US-10-893-802-612
903	815	45.1	352	17	US-10-897-360-612
904	763	42.2	336	15	US-10-471-449-9
905	763	42.2	336	16	US-10-480-172-8
906	761	42.1	319	15	US-10-015-115-22
907	761	42.1	319	15	US-10-015-115-24
908	757	41.9	307	15	US-10-015-115-26
909	726	40.2	336	15	US-10-332-947-53

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Sequence 53, App


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; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-414-657D-47

Query Match 50.2%; Score 907; DB 2; Length 315;
Best Local Similarity 56.3%; Pred. No. 2.9e-82;
Matches 170; Conservative 58; Mismatches 70; Indels 4; Gaps 3;

QY 20 LAALCLF-QGVVRSQDATEPKAMDNVTVROGESATLRCTIDNRVTRVAVLNRSTILYAG 78
DB 17 LRLCLLPTGLPVRSD--FNRGTONTITVRQGDITAILRCVVEDKNSKVAVLNRSGIIFAG 74

QY 79 NDKWCLDPRVLLSNTQTQYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
DB 75 HDKWSLDRVLEKHALEYSLRIQKVDYDEGYSYCSVQTOHEPKTSQVYLLIVQVPPKI 134

QY 139 VEISSDISINEGNNISLCIATGRPEPTVWRHISPKAVGFVSEDEYLEIOGITREQSGD 198
DB 135 SNISSDVTNVEGNNVTLVCMANGRPVITWRHLTPLGRFEGBEYLEILGITREQSGK 194

QY 199 YECASNDVAAPVVRVKVTNYPYIIEAKGTGVPVQKGTLOCEASAVPSAEQWYKD 258
DB 195 YECCAANEVSSADVQKVVTNYPPTITESKNEATTGRQASLKCEASAVPAPDFEYRD 254

QY 259 DKRLTEGKGGKVENRPFSLKLIFFNVSEHDYGNITCVASNKLGHNTNASIMLFGGAYSE 318
DB 255 DTR-INSANGLEIKTEGQSSLTVTNVTEEHYGNITCVAAANKLGVTNASLVLFREGSVRG 313

QY 319 VS 320
DB 314 IN 315

RESULT 14
US-08-414-657D-45
; Sequence 45, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-414-657D-45

Query Match 50.1%; Score 905; DB 2; Length 310;
Best Local Similarity 55.3%; Pred. No. 4.5e-82;
Matches 173; Conservative 59; Mismatches 77; Indels 4; Gaps 3;

QY 31 VRSQDATEPKAMDNVTVROGESATLRCTIDNRVTRVAVLNRSTILYAGNDKWCCLDPRVYL 90
DB 1 VRSVD--FNRGTONTITVRQGDITAILRCVVEDKNSKVAVLNRSGIIFAGHKWSLDRVEL 58

QY 91 LSNTQTQYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEG 150
DB 59 EKRALEYSLRIQKVDYDEGYSYCSVQTOHEPKTSQVYLLIVQVPPKISNSSDVTNVEG 118

QY 151 NNSILTCIATGRPEPTVWRHISPKAVGFVSEDEYLEIOGITREQSGDYECASNDVAAP 210
DB 119 SNVLVCMANGRPVITWRHLTPLGRFEGBEYLEILGITREQSGYKCAANEVSSA 178

QY 211 VVRVKVTNYPYIIEAKGTGVPVQKGTLOCEASAVPSAEQWYKDKRLIEGKGVK 270
DB 179 DVQKVVTNYPPTITESKNEATTGRQASLKCEASAVPAPDFEYRDDTR-INSANGLE 237

QY 271 VENRPFSLKLIFFNVSEHDYGNITCVASNKLGHNTNASIMLFGPGAVSEVNGTSRRACV 330
DB 238 IKSTEGQSSLTVTNVTEEHYGNITCVAAANKLGVTNASLVLFREPGSVIRGI-NGSISLAVPL 296

QY 331 WLLPLLVLHLK 343
DB 297 WLLAASLFCLLSK 309

RESULT 15
US-08-414-657D-44
; Sequence 44, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
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/ TELEFAX: 609-620-3259
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 338 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-09-135-080-8

Query Match 51.1%; Score 923.5; DB 4; Length 338;
Best Local Similarity 55.1%; Pred. No. 7.3e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATFFKAMDNVTVRQGESATLRCTIDNRVTRVAVLNRSTILYAG 78
DB 17 LRLCLLPTGLPVRSD--FNRGTDNITVRQDTAILRCVLEDKSKVAVLNRSGIIFAG 74
QY 79 NDKWCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
DB 75 HDKWSLDPRVLEKHSLEYSRIQKVDYDEGSYTCVQTHPEKTSQVYLIVQVPPKI 134
QY 139 VEISDISINEGNISLTCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREQSGD 198
DB 135 SNISDVTNVEGNSVTLVCMANGREPEVITWRHLTPTGREFEGBEYLEILGITREQSGK 194
QY 199 YECASNDVAAPVRRVKVTNYPPISEAKGTGVPVGOKGTQCEASAVPSAEFQWYKD 258
DB 195 YECCAANEVSSADVQKVTVNYPPTITESKNEATTGQASLKCEASAVPAPDFEWYRD 254
QY 259 DKRLIEGKGGKVKVNRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNASIMLFGPGAVSE 318
DB 255 DTR-INSANGLEIKTEGOSSLTVMVTEHYGNVTCVAANKLGVNASLVLFPGSVRG 313
QY 319 VSGTSTRAGCVMLPLLVHLHLK 343
DB 314 I-NGSISLAVPLWLLAASLLCLSK 337

RESULT 12
US-08-414-657D-46
/ Sequence 46, Application US/08414657D
/ Patent No. 5861283
/ GENERAL INFORMATION:
/ APPLICANT: Levitt, Pat
/ APPLICANT: Pimenta, Aurea
/ APPLICANT: Fischer, Itzhak
/ APPLICANT: Zhukareva, Victoria
/ TITLE OF INVENTION: Limbic System-Associated Membrane
/ TITLE OF INVENTION: Protein and DNA
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dechert Price & Rhoads
/ STREET: 997 Lenox Drive, Building 3, Suite 210
/ CITY: Lawrenceville
/ STATE: NJ
/ COUNTRY: USA
/ ZIP: 08543
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/414,657D
/ FILING DATE: 31-MAR-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bloom, Allen
/ REGISTRATION NUMBER: 29,135

/ REFERENCE/DOCKET NUMBER: 317743-102
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 609-520-3214
/ TELEFAX: 609-520-3259
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 46:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 308 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-414-657D-46

Query Match 50.3%; Score 908; DB 2; Length 308;
Best Local Similarity 56.3%; Pred. No. 2.2e-82;
Matches 170; Conservative 58; Mismatches 70; Indels 4; Gaps 3;

QY 20 LAALCLF-QGVPRSGDATFFKAMDNVTVRQGESATLRCTIDNRVTRVAVLNRSTILYAG 78
DB 10 LRLCLLPTGLPVRSD--FNRGTDNITVRQDTAILRCVLEDKSKVAVLNRSGIIFAG 67
QY 79 NDKWCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
DB 68 HDKWSLDPRVLEKHSLEYSRIQKVDYDEGSYTCVQTHPEKTSQVYLIVQVPPKI 127
QY 139 VEISDISINEGNISLTCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREQSGD 198
DB 128 SNISDVTNVEGNSVTLVCMANGREPEVITWRHLTPTGREFEGBEYLEILGITREQSGK 187
QY 199 YECASNDVAAPVRRVKVTNYPPISEAKGTGVPVGOKGTQCEASAVPSAEFQWYKD 258
DB 188 YECCAANEVSSADVQKVTVNYPPTITESKNEATTGQASLKCEASAVPAPDFEWYRD 247
QY 259 DKRLIEGKGGKVKVNRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNASIMLFGPGAVSE 318
DB 248 DTR-INSANGLEIKTEGOSSLTVMVTEHYGNVTCVAANKLGVNASLVLFPGSVRG 306
QY 319 VS 320
DB 307 IN 308

RESULT 13
US-08-414-657D-47
/ Sequence 47, Application US/08414657D
/ Patent No. 5861283
/ GENERAL INFORMATION:
/ APPLICANT: Levitt, Pat
/ APPLICANT: Pimenta, Aurea
/ APPLICANT: Fischer, Itzhak
/ APPLICANT: Zhukareva, Victoria
/ TITLE OF INVENTION: Limbic System-Associated Membrane
/ TITLE OF INVENTION: Protein and DNA
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dechert Price & Rhoads
/ STREET: 997 Lenox Drive, Building 3, Suite 210
/ CITY: Lawrenceville
/ STATE: NJ
/ COUNTRY: USA
/ ZIP: 08543
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/414,657D
/ FILING DATE: 31-MAR-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-135-080-2

Query Match      51.1%; Score 923.5; DB 4; Length 325;
Best Local Similarity 55.3%; Pred. No. 6.8e-84;
Matches 177; Conservative 60; Mismatches 78; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDAFPKAMDNVTVRQGESATLRCCTIDNRVTRVAVLNRSITLYAG 78
Db 10 LRLLCLLPTGLPVRSD--FNRGTDNITVRQDTAILRCVLEDKNSKVAVLNRSIGIIFAG 67
QY 79 NDKWCLDRVLLSNTQTOYSIEIQNDVDYDEGPTCSVQTDNHPKTSRVLHIVQVSPKI 138
Db 68 HDKWSLDRVLEKHSLEYSRIQKVDYDEGPTCSVQTHPEKTSQVYLIIVQVPPKI 127
QY 139 VEISSDISINGNISLTCIATGRPEPTVWRHISPKAVGVFVSEDEYLEIOGITREQSGD 198
Db 128 SNISSDVTNVEGNSVTLVCMANGREPEVITWRHLTPPTGREFEGEEYLEILGITREQSGK 187
QY 199 YECASNDVAAPVRRVKVTNYPPIYSEAKGTGVPVGQKGTLOCEASAVPSAEFQWYKD 258
Db 188 YECCAANEVSADVKQVKVTNYPPTITESKSNEATTGROASLKCEASAVPAPDFEYRD 247
QY 259 DKRLIEGKKGKVKVNRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTNASIMLFGPGAYSE 318
Db 248 DTR-INSANGLEIKSTEGQSSLTVMVTEEHYGNVTCVAANKLGVNTNASLVLFRPGSVRG 306
QY 319 VSNGTSSRAGCVWLLPLVL 338
Db 307 I-NGSISLAVPLWLLAASLL 325

RESULT 10
US-08-414-657D-60
; Sequence 60, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 60:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-414-657D-60

Query Match      51.1%; Score 923.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 7.3e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDAFPKAMDNVTVRQGESATLRCCTIDNRVTRVAVLNRSITLYAG 78
Db 17 LRLLCLLPTGLPVRSD--FNRGTDNITVRQDTAILRCVLEDKNSKVAVLNRSIGIIFAG 74
QY 79 NDKWCLDRVLLSNTQTOYSIEIQNDVDYDEGPTCSVQTDNHPKTSRVLHIVQVSPKI 138
Db 75 HDKWSLDRVLEKHSLEYSRIQKVDYDEGPTCSVQTHPEKTSQVYLIIVQVPPKI 134
QY 139 VEISSDISINGNISLTCIATGRPEPTVWRHISPKAVGVFVSEDEYLEIOGITREQSGD 198
Db 135 SNISSDVTNVEGNSVTLVCMANGREPEVITWRHLTPPTGREFEGEEYLEILGITREQSGK 194
QY 199 YECASNDVAAPVRRVKVTNYPPIYSEAKGTGVPVGQKGTLOCEASAVPSAEFQWYKD 258
Db 195 YECCAANEVSADVKQVKVTNYPPTITESKSNEATTGROASLKCEASAVPAPDFEYRD 254
QY 259 DKRLIEGKKGKVKVNRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTNASIMLFGPGAYSE 318
Db 255 DTR-INSANGLEIKSTEGQSSLTVMVTEEHYGNVTCVAANKLGVNTNASLVLFRPGSVRG 313
QY 319 VSNGTSSRAGCVWLLPLVL 343
Db 314 I-NGSISLAVPLWLLAASLLCLLSK 337

RESULT 11
US-09-135-080-8
; Sequence 8, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
```


Qy	139	VEISSDISINEGNNISLFCIATGRPEPVTWRHLSPKAVGFVSEDEYLEIQTITRQSGD	198
Db	135	SNISDVTVNEGSNYTLVCMANGRPEPVTWRHLTPGRFBFEGEBEYLEITGITRQSGK	194
Qy	199	YECASNDVAAPVRRVKVTVNYPPYISEAKGTGVPVGQGTLOCEASAVPSAEFQYKD	258
Db	195	YECKAANEVSSADVQKVVTVNYPTTITESKSNEATTGRQASLUKCEASAVPADPFQYRD	254
Qy	259	KRLLEGKGVKVENRPFSLKLIIPNVSEHDYGNVTCVANSKLGHTNASIMLFGCGAVSE	318
Db	255	DYR-INSANGLBIKTEGQSSLTVTNVTTEEYHGYNTCVANKLGVTNASILVLPFQSVRG	313
Qy	319	VNGTSTRRAGCVMLLPVLVHLLK	343
Db	314	I-NGSISLAVPWLWLLAASIFCLLSK	337

RESULT 6

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US-09-135-080-4
; Sequence 4, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-135-080-4

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[illegible]

RESULT 7

```

US-08-414-657D-2
; Sequence 2, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimental, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-414-657D-2

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Db 195 YECCAANEVSSADVQKVTVNVPPTITESKSNKNEATTGQASLKCEASAVPAPDFEWYRD 254
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNASIMLFGPCAYSE 318
Db 255 DTR-INSANGLEIKSTEGQSSLTVTNVTBHHYGNVTCVAANKLGVNASLVLFREGSVRG 313
QY 319 VSGTSSRRAGCWWLLPLLVHLLK 343
Db 314 I-NGSISLAVPLWLLAASLLCLSK 337

RESULT 4

US-08-414-657D-42
; Sequence 42, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-414-657D-42

Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.6e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRVSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVLAWLNRSILYAG 78
Db 17 LRLCLLPTGLPVRSD--FNRGTDNITVRQDITAILRCVVEDKSKVAVLNRSIIFAG 74
QY 79 NDKWCLDPRVLLSNTQTQYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQSPKI 138
Db 75 HDKWSLDRVLEKRAHLEYSRIQKVDVYDEGPTCSVQTDNHPKTSRVHLIVQSPKI 134
QY 139 VEISSDISINEGNNISLTICATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREQSGD 198
Db 135 SNISSDVTYNEGSNVTLCMANGRPFPVITWRHLTPLGREFEGBEYLEILGITREQSGK 194

QY 199 YECASNDVAAPVRRVKVTNVPPIYSEAKGTGVPVQKGTQCEASAVPSAEFQWYKD 258
Db 195 YECCAANEVSSADVQKVTVNVPPTITESKSNKNEATTGQASLKCEASAVPAPDFEWYRD 254
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNASIMLFGPCAYSE 318
Db 255 DTR-INSANGLEIKSTEGQSSLTVTNVTBHHYGNVTCVAANKLGVNASLVLFREGSVRG 313
QY 319 VSGTSSRRAGCWWLLPLLVHLLK 343
Db 314 I-NGSISLAVPLWLLAASLLCLSK 337

RESULT 5

US-08-414-657D-43
; Sequence 43, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-414-657D-43

Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.6e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRVSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVLAWLNRSILYAG 78
Db 17 LRLCLLPTGLPVRSD--FNRGTDNITVRQDITAILRCVVEDKSKVAVLNRSIIFAG 74
QY 79 NDKWCLDPRVLLSNTQTQYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQSPKI 138
Db 75 HDKWSLDRVLEKRAHLEYSRIQKVDVYDEGPTCSVQTDNHPKTSRVHLIVQSPKI 134

1352	111.5	6.2	94	2	US-08-341-843B-30	Sequence 30, Appl	1434	110	6.1	547	3	US-08-296-749-1	Sequence 1, Appli
1353	111.5	6.2	94	2	US-08-427-497E-35	Sequence 35, Appl	1435	110	6.1	547	4	US-08-314-369-1	Sequence 1, Appli
1354	111.5	6.2	284	4	US-08-961-309-70	Sequence 70, Appl	1436	110	6.1	771	3	US-08-434-000A-8	Sequence 8, Appli
1355	111.5	6.2	431	4	US-09-773-877B-27	Sequence 27, Appl	1437	110	6.1	771	3	US-09-312-157-8	Sequence 8, Appli
1356	111.5	6.2	458	4	US-09-773-877B-26	Sequence 26, Appl	1438	110	6.1	771	3	US-09-717-888-8	Sequence 8, Appli
1357	111.5	6.2	480	2	US-08-425-989B-11	Sequence 11, Appl	1439	109.5	6.1	274	4	US-08-961-309-66	Sequence 66, Appl
1358	111.5	6.2	567	3	US-09-560-633-7	Sequence 7, Appli	1440	109.5	6.1	453	6	5284931-3	Patent No. 5284931
1359	111.5	6.2	567	3	US-09-173-151A-24	Sequence 24, Appl	1441	109.5	6.1	453	6	5284931-3	Patent No. 5284931
1360	111.5	6.2	567	3	US-09-032-337-39	Sequence 39, Appl	1442	109.5	6.1	505	3	US-08-318-039A-1	Sequence 1, Appli
1361	111	6.1	275	3	US-08-463-903-6	Sequence 6, Appli	1443	109.5	6.1	505	3	US-08-318-039A-1	Sequence 1, Appli
1362	111	6.1	275	3	US-08-463-903-8	Sequence 8, Appli	1444	109.5	6.1	505	3	US-08-318-039A-1	Sequence 1, Appli
1363	111	6.1	275	3	US-07-935-695-6	Sequence 6, Appli	1445	109.5	6.1	505	3	US-08-227-496C-19	Sequence 19, Appl
1364	111	6.1	275	3	US-07-935-695-8	Sequence 8, Appli	1446	109.5	6.1	505	3	US-08-435-588A-1	Sequence 1, Appli
1365	111	6.1	280	3	US-08-463-903-10	Sequence 10, Appl	1447	109.5	6.1	505	3	US-09-240-915-6	Sequence 6, Appli
1366	111	6.1	280	3	US-07-935-695-10	Sequence 10, Appl	1448	109.5	6.1	505	3	US-09-591-435-6	Sequence 6, Appli
1367	111	6.1	282	3	US-08-463-903-12	Sequence 12, Appl	1449	109.5	6.1	507	1	US-08-464-083-14	Sequence 14, Appl
1368	111	6.1	282	3	US-07-935-695-12	Sequence 12, Appl	1450	109.5	6.1	507	2	US-08-469-587A-14	Sequence 14, Appl
1369	111	6.1	321	3	US-09-361-434-17	Sequence 17, Appl	1451	109.5	6.1	531	2	US-08-789-078-3	Sequence 3, Appli
1370	111	6.1	321	3	US-09-361-434-22	Sequence 22, Appl	1452	109.5	6.1	531	2	US-08-752-633-3	Sequence 3, Appli
1371	111	6.1	321	3	US-09-635-025-17	Sequence 17, Appl	1453	109.5	6.1	531	5	PCT-US95-04886-3	Sequence 3, Appli
1372	111	6.1	321	3	US-09-635-025-22	Sequence 22, Appl	1454	109.5	6.1	532	2	US-08-483-389-118	Sequence 118, Appl
1373	111	6.1	398	1	US-08-091-519-2	Sequence 2, Appli	1455	109.5	6.1	532	2	US-08-689-870-12	Sequence 12, Appl
1374	111	6.1	398	1	US-08-442-043A-2	Sequence 2, Appli	1456	109.5	6.1	532	3	US-09-003-490A-87	Sequence 87, Appl
1375	111	6.1	398	3	US-09-173-151A-26	Sequence 26, Appl	1457	109.5	6.1	532	6	5284931-2	Patent No. 5284931
1376	111	6.1	398	4	US-09-461-908-2	Sequence 2, Appli	1458	109.5	6.1	532	6	5284931-2	Patent No. 5284931
1377	111	6.1	398	4	US-08-441-893A-2	Sequence 2, Appli	1459	109	6.0	170	4	US-09-270-767-43106	Sequence 43106, A
1378	111	6.1	398	4	US-09-579-845-4	Sequence 4, Appli	1460	109	6.0	282	3	US-08-463-903-15	Sequence 15, Appl
1379	111	6.1	398	4	US-08-406-824A-8	Sequence 8, Appli	1461	109	6.0	282	3	US-07-935-695-15	Sequence 15, Appl
1380	111	6.1	398	4	US-09-921-667-8	Sequence 8, Appli	1462	109	6.0	285	3	US-08-463-903-22	Sequence 22, Appl
1381	111	6.1	398	5	PCT-US91-03478-2	Sequence 2, Appli	1463	109	6.0	285	3	US-07-935-695-22	Sequence 22, Appl
1382	111	6.1	418	4	US-09-949-016-6278	Sequence 6278, Ap	1464	108	6.0	474	4	US-09-828-935B-17	Sequence 17, Appl
1383	111	6.1	467	4	US-08-030-175-41	Sequence 41, Appl	1465	109	6.0	1140	4	US-09-517-605-3	Sequence 3, Appli
1384	111	6.1	467	4	US-08-030-175-42	Sequence 42, Appl	1466	108	6.0	269	4	US-10-000-489-78	Sequence 78, Appl
1385	111	6.1	479	4	US-09-723-368-2	Sequence 2, Appli	1467	108	6.0	319	4	US-09-910-174B-12	Sequence 12, Appl
1386	111	6.1	479	4	US-09-949-016-6278	Sequence 6278, Ap	1468	108	6.0	319	4	US-09-620-461-12	Sequence 12, Appl
1387	111	6.1	522	4	US-09-896-537A-2	Sequence 2, Appli	1469	108	6.0	474	4	US-08-768-964-12	Sequence 12, Appl
1388	111	6.1	522	4	US-08-896-537A-2	Sequence 2, Appli	1470	107.5	6.0	199	2	US-08-768-964-12	Sequence 12, Appl
1389	111	6.1	729	2	US-08-070-165F-6	Sequence 6, Appli	1471	107.5	6.0	199	3	US-09-005-299-12	Sequence 12, Appl
1390	111	6.1	729	2	US-08-885-418-6	Sequence 6, Appli	1472	107.5	6.0	199	3	US-09-515-431-12	Sequence 12, Appl
1391	110.5	6.1	141	4	US-09-858-664A-15	Sequence 15, Appl	1473	107.5	6.0	263	2	US-08-768-964-2	Sequence 2, Appli
1392	110.5	6.1	141	4	US-10-274-978-16	Sequence 16, Appl	1474	107.5	6.0	263	2	US-09-005-299-2	Sequence 2, Appli
1393	110.5	6.1	141	4	US-10-697-263-16	Sequence 16, Appl	1475	107.5	6.0	263	3	US-09-005-299-2	Sequence 2, Appli
1394	110.5	6.1	260	3	US-08-463-903-2	Sequence 2, Appli	1476	107.5	6.0	264	1	US-08-323-445A-8	Sequence 8, Appli
1395	110.5	6.1	260	3	US-07-935-695-2	Sequence 2, Appli	1477	107.5	6.0	264	1	US-08-515-903A-8	Sequence 8, Appli
1396	110.5	6.1	260	4	US-08-961-309-64	Sequence 64, Appl	1478	107.5	6.0	264	5	PCT-US95-12840-8	Sequence 8, Appli
1397	110.5	6.1	275	3	US-08-463-903-17	Sequence 17, Appl	1479	107	5.9	318	4	US-09-656-952-2	Sequence 2, Appli
1398	110.5	6.1	275	3	US-07-935-695-17	Sequence 17, Appl	1480	107	5.9	344	4	US-09-656-952-19	Sequence 19, Appl
1399	110.5	6.1	584	4	US-09-910-174B-16	Sequence 16, Appl	1481	107	5.9	394	4	US-09-656-952-20	Sequence 20, Appl
1400	110.5	6.1	584	4	US-08-620-461-16	Sequence 16, Appl	1482	106.5	5.9	248	6	5455030-11	Patent No. 5455030
1401	110.5	6.1	601	2	US-08-795-868-16	Sequence 16, Appl	1483	106.5	5.9	248	6	5455030-11	Patent No. 5455030
1402	110.5	6.1	602	3	US-09-303-069-16	Sequence 16, Appl	1484	106.5	5.9	271	2	US-08-400-115-4	Sequence 4, Appli
1403	110.5	6.1	602	3	US-09-134-250-16	Sequence 16, Appl	1485	106	5.9	244	2	US-08-392-338A-13	Sequence 13, Appl
1413	110	6.1	242	2	US-08-224-591-14	Sequence 14, Appl	1486	106	5.9	244	3	US-09-166-750-13	Sequence 13, Appl
1414	110	6.1	242	2	US-08-392-338A-23	Sequence 23, Appl	1487	106	5.9	244	3	US-09-166-093-13	Sequence 13, Appl
1415	110	6.1	242	2	US-08-926-789-14	Sequence 14, Appl	1488	106	5.9	244	3	US-09-172-019-13	Sequence 13, Appl
1416	110	6.1	242	3	US-09-166-750-23	Sequence 23, Appl	1489	106	5.9	244	3	US-09-166-094-13	Sequence 13, Appl
1417	110	6.1	242	3	US-09-166-093-23	Sequence 23, Appl	1490	106	5.9	244	4	US-09-443-213-13	Sequence 13, Appl
1418	110	6.1	242	3	US-09-172-019-23	Sequence 23, Appl	1491	105.5	5.8	231	1	US-08-681-432-1	Sequence 1, Appli
1419	110	6.1	242	3	US-09-166-094-23	Sequence 23, Appl	1492	105.5	5.8	337	1	US-08-442-043A-18	Sequence 18, Appl
1420	110	6.1	242	4	US-09-443-213-23	Sequence 23, Appl	1493	105.5	5.8	337	3	US-09-560-639-6	Sequence 6, Appli
1421	110	6.1	244	5	PCT-US93-11138-14	Sequence 14, Appl	1494	105.5	5.8	337	4	US-08-441-893A-18	Sequence 18, Appl
1422	110	6.1	547	1	US-08-314-615-1	Sequence 1, Appli	1495	105.5	5.8	342	4	US-09-032-337-41	Sequence 41, Appl
1423	110	6.1	547	1	US-08-314-362-1	Sequence 1, Appli	1496	105	5.8	63	4	US-09-397-243D-8	Sequence 8, Appli
1424	110	6.1	547	1	US-08-433-010-1	Sequence 1, Appli	1497	105	5.8	63	4	US-09-397-243D-10	Sequence 10, Appl
1425	110	6.1	547	1	US-08-482-882-1	Sequence 1, Appli	1498	105	5.8	269	4	US-09-949-016-6121	Sequence 6121, Ap
1426	110	6.1	547	2	US-08-483-389-1	Sequence 1, Appli	1499	105	5.8	276	4	US-09-943-016-7261	Sequence 7261, Ap
1427	110	6.1	547	2	US-08-487-113D-1	Sequence 1, Appli	1500	105	5.8	512	4	US-08-999-689A-7	Sequence 7, Appli
1428	110	6.1	547	2	US-08-473-503-1	Sequence 1, Appli							
1429	110	6.1	547	2	US-08-483-932-1	Sequence 1, Appli							
1430	110	6.1	547	2	US-08-720-420A-1	Sequence 1, Appli							
1431	110	6.1	547	3	US-08-714-017-1	Sequence 1, Appli							
1432	110	6.1	547	3	US-08-863-790-1	Sequence 1, Appli							
1433	110	6.1	547	3	US-08-475-680-1	Sequence 1, Appli							

ALIGNMENTS

RESULT 1

1188	120.5	6.7	236	6	5455030-7	Patent No. 5455030	1279	117	6.5	1665	4	US-09-858-664A-2	Sequence 2, Appli
1189	120.5	6.7	236	6	5455030-7	Patent No. 5455030	1280	117	6.5	1665	4	US-10-274-978-2	Sequence 2, Appli
1190	120.5	6.7	193	4	US-09-397-243D-4	Sequence 4, Appli	1281	117	6.5	1665	4	US-10-697-263-2	Sequence 2, Appli
1191	120	6.6	205	3	US-09-462-270-4	Sequence 4, Appli	1282	116.5	6.5	1665	2	US-08-332-562A-83	Sequence 83, Appli
1192	120	6.6	328	4	US-09-949-016-6428	Sequence 4828, Ap	1283	116.5	6.5	315	4	US-09-949-016-7014	Sequence 7014, Ap
1193	120	6.6	329	4	US-09-149-476-483	Sequence 483, Ap	1284	116.5	6.5	315	4	US-08-227-496C-15	Sequence 15, Appl
1194	120	6.6	332	4	US-09-949-016-7327	Sequence 7327, Ap	1285	116.5	6.5	680	3	US-09-419-788-19	Sequence 19, Appl
1195	120	6.6	361	4	US-09-270-767-45128	Sequence 45128, A	1286	116	6.4	1060	4	US-08-833-488B-14	Sequence 14, Appl
1196	119.5	6.6	197	3	US-08-833-488B-28	Sequence 28, Appl	1287	116	6.4	731	1	US-07-921-807B-5	Sequence 5, Appli
1197	119.5	6.6	253	3	US-08-833-488B-20	Sequence 20, Appl	1288	116	6.4	731	1	US-08-441-994A-5	Sequence 5, Appli
1207	119.5	6.6	477	4	US-09-949-016-9192	Sequence 9192, Ap	1289	116	6.4	731	3	US-08-439-992A-3	Sequence 3, Appli
1208	119.5	6.6	477	4	US-09-949-016-9194	Sequence 9194, Ap	1290	116	6.4	879	1	US-08-554-612C-1	Sequence 1, Appli
1209	119.5	6.6	477	4	US-09-949-016-9195	Sequence 9195, Ap	1291	116	6.4	993	1	US-08-183-211-2	Sequence 2, Appli
1210	119.5	6.6	477	4	US-09-949-016-9196	Sequence 9196, Ap	1292	116	6.4	993	5	PCT-US95-00176A-2	Sequence 2, Appli
1211	119.5	6.6	477	4	US-09-949-016-9197	Sequence 9197, Ap	1293	115.5	6.4	173	3	US-08-833-488B-31	Sequence 31, Appl
1212	119.5	6.6	477	4	US-09-949-016-9198	Sequence 9198, Ap	1294	115.5	6.4	229	3	US-08-833-488B-24	Sequence 24, Appl
1213	119.5	6.6	477	4	US-09-949-016-9199	Sequence 9199, Ap	1295	115.5	6.4	248	1	US-08-323-445A-6	Sequence 6, Appli
1214	119.5	6.6	505	3	US-09-240-915-3	Sequence 3, Appli	1296	115.5	6.4	248	1	US-08-515-903A-6	Sequence 6, Appli
1215	119.5	6.6	505	3	US-09-591-435-3	Sequence 3, Appli	1297	115.5	6.4	248	5	PCT-US95-12840-6	Sequence 6, Appli
1216	119.5	6.6	261	4	US-08-899-634C-2	Sequence 2, Appli	1298	115.5	6.4	530	3	US-08-477-450B-4	Sequence 4, Appli
1217	119	6.6	330	2	US-08-525-864A-4	Sequence 4, Appli	1299	115.5	6.4	530	3	US-08-379-516-4	Sequence 4, Appli
1218	119	6.6	365	4	US-08-899-634C-4	Sequence 4, Appli	1300	115.5	6.4	530	3	US-08-329-916-4	Sequence 4, Appli
1219	119	6.6	754	2	US-08-525-864A-2	Sequence 2, Appli	1301	115.5	6.4	530	3	US-08-485-372A-4	Sequence 4, Appli
1220	119	6.6	910	4	US-09-313-942-28	Sequence 28, Appl	1302	115.5	6.4	530	3	US-09-409-006A-4	Sequence 4, Appli
1221	119	6.6	969	4	US-09-949-016-8059	Sequence 8059, Ap	1303	115.5	6.4	530	4	US-08-484-681-4	Sequence 4, Appli
1222	119	6.6	553	2	US-08-263-911-7	Sequence 7, Appli	1304	115.5	6.4	530	4	US-09-766-995-4	Sequence 4, Appli
1223	118.5	6.6	668	4	US-09-949-016-8139	Sequence 8139, Ap	1305	115.5	6.4	530	5	PCT-US93-07422-4	Sequence 4, Appli
1224	118.5	6.6	2860	2	US-08-826-267-2	Sequence 2, Appli	1306	115	6.4	318	6	5223394-11	Patent No. 5223394
1225	118.5	6.6	300	1	US-07-640-029-5	Sequence 5, Appli	1307	115	6.4	318	6	5223394-11	Patent No. 5223394
1226	118	6.5	300	1	US-08-439-992A-5	Sequence 5, Appli	1308	114.5	6.3	139	1	US-08-168-091A-35	Sequence 35, Appl
1227	118	6.5	300	1	US-08-439-992A-5	Sequence 5, Appli	1309	114.5	6.3	365	3	US-08-928-383B-23	Sequence 23, Appl
1228	118	6.5	993	1	US-08-222-239-4	Sequence 4, Appli	1310	114.5	6.3	365	3	US-08-928-383B-24	Sequence 24, Appl
1229	118	6.5	993	2	US-08-434-878-4	Sequence 4, Appli	1311	114.5	6.3	455	4	US-09-949-016-6949	Sequence 6949, Ap
1230	118	6.5	993	5	PCT-US95-03718-4	Sequence 4, Appli	1312	114	6.3	302	1	US-07-640-029-6	Sequence 6, Appli
1231	117.5	6.5	191	4	US-09-270-767-33678	Sequence 33678, A	1313	114	6.3	302	1	US-07-921-807B-8	Sequence 8, Appli
1232	117.5	6.5	246	4	US-09-270-767-48895	Sequence 48895, A	1314	114	6.3	302	1	US-08-441-944A-8	Sequence 8, Appli
1233	117.5	6.5	246	4	US-09-336-536-31	Sequence 31, Appl	1315	114	6.3	302	3	US-08-439-992A-6	Sequence 6, Appli
1234	117.5	6.5	336	1	US-07-904-073-2	Sequence 2, Appli	1316	114	6.3	467	3	US-09-046-736-2	Sequence 2, Appli
1235	117.5	6.5	336	1	US-07-904-071-2	Sequence 2, Appli	1317	113.5	6.3	262	1	US-08-323-445A-4	Sequence 4, Appli
1236	117.5	6.5	336	1	US-08-442-043A-16	Sequence 16, Appl	1318	113.5	6.3	262	1	US-08-515-903A-4	Sequence 4, Appli
1237	117.5	6.5	336	4	US-08-441-893A-16	Sequence 16, Appl	1319	113.5	6.3	262	5	PCT-US95-12840-4	Sequence 4, Appli
1238	117.5	6.5	365	4	US-09-336-536-40	Sequence 40, Appl	1320	113.5	6.3	307	3	US-08-996-338-25	Sequence 25, Appl
1239	117.5	6.5	569	1	US-07-821-716-2	Sequence 2, Appli	1321	113.5	6.3	307	4	US-09-556-972-25	Sequence 25, Appl
1240	117.5	6.5	569	2	US-08-381-603-2	Sequence 2, Appli	1322	113.5	6.3	455	4	US-09-949-016-11026	Sequence 11026, A
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1243	117.5	6.5	569	3	US-08-173-151A-31	Sequence 31, Appl	1325	113.5	6.3	519	3	US-08-996-338-21	Sequence 21, Appl
1244	117.5	6.5	569	4	US-08-466-932A-6	Sequence 2, Appli	1326	113.5	6.3	519	4	US-09-556-972-21	Sequence 21, Appl
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1246	117.5	6.5	569	4	US-09-949-016-6000	Sequence 6000, Ap	1328	113.5	6.3	537	3	US-09-110-618-4	Sequence 4, Appli
1247	117.5	6.5	569	5	PCT-US94-02414-2	Sequence 2, Appli	1329	113.5	6.3	537	3	US-09-173-151A-29	Sequence 29, Appl
1248	117.5	6.5	569	5	PCT-US96-08899-2	Sequence 2, Appli	1330	113.5	6.3	537	4	US-09-578-178-4	Sequence 4, Appli
1249	117.5	6.5	588	4	US-09-949-016-8572	Sequence 8572, Ap	1331	113.5	6.3	537	4	US-09-577-806-4	Sequence 4, Appli
1250	117	6.5	264	4	US-09-270-767-33115	Sequence 33115, A	1332	113.5	6.3	537	4	US-09-621-502-8	Sequence 8, Appli
1251	117	6.5	264	4	US-09-270-767-48332	Sequence 48332, A	1333	113.5	6.3	547	1	US-08-473-981A-6	Sequence 6, Appli
1252	117	6.5	407	3	US-08-753-007A-6	Sequence 6, Appli	1334	113.5	6.3	547	2	US-08-474-087-6	Sequence 6, Appli
1253	117	6.5	407	3	US-09-398-496-6	Sequence 6, Appli	1335	113	6.3	273	4	US-09-270-767-32843	Sequence 32843, A
1254	117	6.5	708	3	US-09-131-628-2	Sequence 2, Appli	1336	113	6.3	273	4	US-09-270-767-48060	Sequence 48060, A
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1256	117	6.5	733	1	US-07-640-029-4	Sequence 4, Appli	1338	113	6.3	458	4	US-09-773-877B-22	Sequence 22, Appl
1257	117	6.5	733	1	US-07-921-807B-6	Sequence 6, Appli	1339	112.5	6.2	365	3	US-08-928-383B-26	Sequence 26, Appl
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1260	117	6.5	825	1	US-07-912-952-2	Sequence 2, Appli	1342	112.5	6.2	414	4	US-10-697-263-14	Sequence 14, Appl
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1262	117	6.5	885	1	US-09-919-497-52	Sequence 52, Appl	1344	112.5	6.2	503	4	US-09-944-807-4	Sequence 4, Appli
1263	117	6.5	894	1	US-08-372-892-2	Sequence 2, Appli	1345	112	6.2	170	4	US-09-245-764-6	Sequence 6, Appli
1264	117	6.5	894	1	US-08-445-640-34	Sequence 34, Appl	1346	112	6.2	181	3	US-08-753-007A-4	Sequence 4, Appli
1265	117	6.5	894	1	US-08-170-558-34	Sequence 34, Appl	1347	112	6.2	181	3	US-09-398-496-4	Sequence 4, Appli
1266	117	6.5	894	3	US-08-447-314-34	Sequence 34, Appl	1348	112	6.2	247	6	5455030-9	Patent No. 5455030
1267	117	6.5	894	3	US-08-445-461-34	Sequence 34, Appl	1349	112	6.2	247	6	5455030-9	Patent No. 5455030
1268	117	6.5	894	4	US-09-223-490-34	Sequence 34, Appl	1350	112	6.2	605	3	US-08-753-007A-2	Sequence 2, Appli
1269	117	6.5	894	4	US-09-949-016-7595	Sequence 7595, Ap	1351	112	6.2	605	3	US-09-398-496-2	Sequence 2, Appli

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1034	123.5	6.8	645	1	US-08-339-517-4	Sequence 4, Appli	1107	122.5	6.8	635	4	US-08-467-602-231	Sequence 231, App
1035	123.5	6.8	645	2	US-08-456-241-27	Sequence 27, Appl	1108	122.5	6.8	635	4	US-08-411-295F-157	Sequence 157, App
1036	123.5	6.8	645	3	US-09-020-880-93	Sequence 93, Appl	1109	122.5	6.8	637	4	US-08-467-602-258	Sequence 258, App
1037	123.5	6.8	645	3	US-09-101-544-93	Sequence 93, Appl	1110	122.5	6.8	637	4	US-08-411-295F-184	Sequence 184, App
1038	123.5	6.8	645	4	US-09-097-681-3	Sequence 3, Appli	1111	122.5	6.8	640	4	US-08-467-603-256	Sequence 256, App
1039	123.5	6.8	645	5	PCT-US92-04295A-27	Sequence 27, Appl	1112	122.5	6.8	640	4	US-08-411-295F-182	Sequence 182, App
1040	123.5	6.8	732	1	US-07-847-743B-9	Sequence 9, Appli	1113	122.5	6.8	645	3	US-08-753-007A-10	Sequence 10, Appl
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1042	123.5	6.8	732	2	US-08-456-241-9	Sequence 9, Appli	1115	122.5	6.8	646	4	US-08-467-602-270	Sequence 270, App
1043	123.5	6.8	732	5	PCT-US92-04295A-9	Sequence 9, Appli	1116	122.5	6.8	646	4	US-08-411-295F-196	Sequence 196, App
1044	123	6.8	321	4	US-09-254-465A-2	Sequence 2, Appli	1117	122.5	6.8	649	4	US-08-467-602-267	Sequence 267, App
1045	123	6.8	321	4	US-09-953-499-2	Sequence 2, Appli	1118	122.5	6.8	649	4	US-08-411-295F-193	Sequence 193, App
1046	123	6.8	354	6	5169835-4	Patent No. 5169835	1119	122.5	6.8	650	4	US-08-411-295F-190	Sequence 190, App
1047	123	6.8	354	6	5169835-4	Sequence 9, Appli	1120	122.5	6.8	650	4	US-08-467-602-217	Sequence 217, App
1048	123	6.8	553	2	US-08-263-911-9	Sequence 35, Appl	1121	122.5	6.8	653	4	US-08-467-602-212	Sequence 212, App
1049	123	6.8	668	3	US-09-173-151A-35	Sequence 2, Appli	1122	122.5	6.8	653	4	US-08-411-295F-138	Sequence 138, App
1050	123	6.8	821	1	US-08-339-578-2	Sequence 380, App	1123	122.5	6.8	659	4	US-08-467-602-229	Sequence 229, App
1051	122.5	6.8	133	4	US-08-467-602-380	Sequence 18, Appl	1124	122.5	6.8	659	4	US-08-411-295F-155	Sequence 155, App
1052	122.5	6.8	161	1	US-08-096-277-18	Sequence 18, Appl	1125	122.5	6.8	660	4	US-08-467-602-264	Sequence 264, App
1053	122.5	6.8	161	3	US-08-550-815-18	Sequence 18, Appl	1126	122.5	6.8	660	4	US-08-411-295F-190	Sequence 190, App
1054	122.5	6.8	161	3	US-08-703-089-18	Sequence 18, Appl	1127	122.5	6.8	662	4	US-08-467-602-226	Sequence 226, App
1055	122.5	6.8	207	4	US-08-467-602-219	Sequence 219, App	1128	122.5	6.8	662	4	US-08-411-295F-152	Sequence 152, App
1056	122.5	6.8	207	4	US-08-411-295F-145	Sequence 145, App	1129	122.5	6.8	669	1	US-07-847-743B-13	Sequence 13, Appl
1057	122.5	6.8	210	4	US-08-467-602-215	Sequence 215, App	1130	122.5	6.8	669	1	US-08-456-201-8	Sequence 8, Appli
1058	122.5	6.8	210	4	US-08-411-295F-141	Sequence 141, App	1131	122.5	6.8	669	1	US-08-456-201-13	Sequence 13, Appl
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1060	122.5	6.8	230	4	US-08-411-295F-149	Sequence 149, App	1133	122.5	6.8	669	2	US-08-456-241-8	Sequence 8, Appli
1061	122.5	6.8	241	4	US-08-467-602-261	Sequence 261, App	1134	122.5	6.8	669	2	US-08-411-295F-185	Sequence 185, App
1062	122.5	6.8	241	4	US-08-411-295F-187	Sequence 187, App	1135	122.5	6.8	669	2	US-08-440-401-13	Sequence 13, Appl
1063	122.5	6.8	244	4	US-08-467-602-257	Sequence 257, App	1136	122.5	6.8	669	2	US-08-419-878B-11	Sequence 11, Appl
1064	122.5	6.8	244	4	US-08-411-295F-183	Sequence 183, App	1137	122.5	6.8	669	3	US-09-173-480-11	Sequence 11, Appl
1065	122.5	6.8	264	4	US-08-467-602-265	Sequence 265, App	1138	122.5	6.8	669	4	US-08-467-602-273	Sequence 273, App
1066	122.5	6.8	264	4	US-08-411-295F-191	Sequence 191, App	1139	122.5	6.8	669	4	US-08-411-295F-139	Sequence 139, App
1067	122.5	6.8	386	4	US-08-467-602-218	Sequence 218, App	1140	122.5	6.8	669	5	PCT-US92-04295A-8	Sequence 8, Appli
1068	122.5	6.8	386	4	US-08-411-295F-144	Sequence 144, App	1141	122.5	6.8	669	5	PCT-US92-04295A-13	Sequence 13, Appl
1069	122.5	6.8	389	4	US-08-467-602-213	Sequence 213, App	1142	122.5	6.8	673	4	US-08-411-295F-146	Sequence 146, App
1070	122.5	6.8	389	4	US-08-411-295F-139	Sequence 139, App	1143	122.5	6.8	673	4	US-08-467-602-220	Sequence 220, App
1071	122.5	6.8	395	4	US-08-467-602-227	Sequence 227, App	1144	122.5	6.8	682	4	US-08-411-295F-158	Sequence 158, App
1072	122.5	6.8	395	4	US-08-411-295F-153	Sequence 153, App	1145	122.5	6.8	682	4	US-08-467-602-259	Sequence 259, App
1073	122.5	6.8	398	4	US-08-467-602-224	Sequence 224, App	1146	122.5	6.8	684	4	US-08-411-295F-188	Sequence 188, App
1074	122.5	6.8	398	4	US-08-411-295F-150	Sequence 150, App	1147	122.5	6.8	684	4	US-08-467-602-262	Sequence 262, App
1075	122.5	6.8	409	4	US-08-467-602-221	Sequence 221, App	1148	122.5	6.8	684	4	US-08-411-295F-194	Sequence 194, App
1076	122.5	6.8	409	4	US-08-411-295F-147	Sequence 147, App	1149	122.5	6.8	687	4	US-08-467-602-254	Sequence 254, App
1077	122.5	6.8	418	4	US-08-467-602-230	Sequence 230, App	1150	122.5	6.8	687	4	US-08-411-295F-180	Sequence 180, App
1078	122.5	6.8	418	4	US-08-411-295F-156	Sequence 156, App	1151	122.5	6.8	693	4	US-08-467-602-271	Sequence 271, App
1079	122.5	6.8	420	4	US-08-467-602-260	Sequence 260, App	1152	122.5	6.8	693	4	US-08-411-295F-197	Sequence 197, App
1080	122.5	6.8	420	4	US-08-411-295F-186	Sequence 186, App	1153	122.5	6.8	696	4	US-08-467-602-268	Sequence 268, App
1081	122.5	6.8	422	3	US-08-753-007A-9	Sequence 9, Appli	1154	122.5	6.8	696	4	US-08-411-295F-194	Sequence 194, App
1082	122.5	6.8	423	3	US-09-398-496-9	Sequence 9, Appli	1155	122.5	6.8	707	4	US-08-467-602-262	Sequence 262, App
1083	122.5	6.8	423	4	US-08-467-602-255	Sequence 255, App	1156	122.5	6.8	707	4	US-08-411-295F-188	Sequence 188, App
1084	122.5	6.8	423	4	US-08-411-295F-181	Sequence 181, App	1157	122.5	6.8	716	4	US-08-467-602-274	Sequence 274, App
1085	122.5	6.8	429	4	US-08-467-602-269	Sequence 269, App	1158	122.5	6.8	716	4	US-08-411-295F-200	Sequence 200, App
1086	122.5	6.8	429	4	US-08-411-295F-195	Sequence 195, App	1159	122	6.8	146	4	US-09-270-767-33187	Sequence 33187, A
1087	122.5	6.8	432	4	US-08-467-602-266	Sequence 266, App	1160	122	6.8	357	4	US-09-949-016-9074	Sequence 9074, Ap
1088	122.5	6.8	432	4	US-08-411-295F-192	Sequence 192, App	1161	122	6.8	363	4	US-09-949-016-11040	Sequence 11040, A
1089	122.5	6.8	443	4	US-08-467-602-263	Sequence 263, App	1162	122	6.8	365	4	US-09-949-016-9075	Sequence 9075, Ap
1090	122.5	6.8	443	4	US-08-411-295F-189	Sequence 189, App	1163	122	6.8	371	4	US-09-949-016-9073	Sequence 9073, Ap
1091	122.5	6.8	452	4	US-08-467-602-272	Sequence 272, App	1164	122	6.8	421	4	US-09-563-611C-36	Sequence 36, Appl
1092	122.5	6.8	452	4	US-08-411-295F-198	Sequence 198, App	1165	122	6.8	469	3	US-09-398-496-8	Sequence 8, Appli
1093	122.5	6.8	603	4	US-08-467-602-216	Sequence 216, App	1166	122	6.8	469	3	US-08-753-007A-32	Sequence 32, Appl
1094	122.5	6.8	603	4	US-08-411-295F-142	Sequence 142, App	1167	122	6.8	647	3	US-09-398-496-32	Sequence 32, Appl
1095	122.5	6.8	606	4	US-08-467-602-214	Sequence 214, App	1168	122	6.8	647	3	US-08-168-091A-4	Sequence 4, Appli
1096	122.5	6.8	606	4	US-08-411-295F-140	Sequence 140, App	1169	121.5	6.7	231	1	US-09-270-767-44618	Sequence 44618, A
1097	122.5	6.8	612	4	US-08-467-602-228	Sequence 228, App	1170	121.5	6.7	286	4	US-08-979-424-1	Sequence 1, Appli
1098	122.5	6.8	612	4	US-08-411-295F-154	Sequence 154, App	1171	121.5	6.7	390	2	US-07-921-807B-7	Sequence 7, Appli
1099	122.5	6.8	615	4	US-08-467-602-225	Sequence 225, App	1181	121	6.7	302	1	US-08-441-944A-7	Sequence 7, Appli
1100	122.5	6.8	615	4	US-08-411-295F-151	Sequence 151, App	1182	121	6.7	302	1	US-09-910-174B-28	Sequence 28, Appl
1101	122.5	6.8	625	1	US-07-847-743B-26	Sequence 26, Appl	1183	121	6.7	315	4	US-09-620-461-28	Sequence 28, Appl
1102	122.5	6.8	625	1	US-08-456-201-26	Sequence 26, Appl	1184	121	6.7	315	4	US-08-168-091A-33	Sequence 33, Appl
1103	122.5	6.8	625	2	US-08-456-241-26	Sequence 26, Appl	1185	120.5	6.7	165	1	US-08-833-488B-4	Sequence 4, Appli
1104	122.5	6.8	625	5	PCT-US92-04295A-26	Sequence 26, Appl	1186	120.5	6.7	197	3	US-08-833-488B-9	Sequence 9, Appli
1105	122.5	6.8	626	4	US-08-467-602-222	Sequence 222, App	1187	120.5	6.7	197	3		

887	131	7.3	782	4	US-09-684-708A-21	Sequence 21, Appl	960	127	7.0	992	4	US-09-872-136B-2	Sequence 2, Appl
888	131	7.3	1090	4	US-09-866-510-14	Sequence 14, Appl	961	127	7.0	992	5	PCT-US92-0250-2	Sequence 2, Appl
889	131	7.3	1106	1	US-08-180-195-2	Sequence 2, Appl	962	127	7.0	992	5	PCT-US92-05401-2	Sequence 2, Appl
890	131	7.3	1106	1	US-08-168-917-2	Sequence 2, Appl	963	127	7.0	992	5	PCT-US92-09893-2	Sequence 2, Appl
891	131	7.3	1106	1	US-08-477-329-2	Sequence 2, Appl	964	126.5	7.0	365	2	US-08-979-424-3	Sequence 2, Appl
892	131	7.3	1106	2	US-08-475-458-2	Sequence 2, Appl	965	126.5	7.0	365	3	US-09-273-496-2	Sequence 2, Appl
893	131	7.3	1106	2	US-08-460-510-2	Sequence 2, Appl	966	126.5	7.0	365	4	US-09-949-016-6064	Sequence 6064, Ap
894	131	7.3	1106	2	US-08-460-490-2	Sequence 2, Appl	967	126	7.0	277	4	US-09-354-151-3	Sequence 3, Appl
895	131	7.3	1106	3	US-08-980-400-2	Sequence 2, Appl	968	126	7.0	477	2	US-08-359-705B-4	Sequence 4, Appl
896	131	7.3	1106	3	US-08-462-728-4	Sequence 4, Appl	969	126	7.0	477	2	US-08-286-846A-4	Sequence 4, Appl
897	131	7.3	1106	3	US-09-583-459A-2	Sequence 2, Appl	970	126	7.0	477	2	US-08-457-880A-4	Sequence 4, Appl
898	131	7.3	1106	3	US-09-583-210-2	Sequence 2, Appl	971	126	7.0	477	3	US-08-444-622A-4	Sequence 4, Appl
899	131	7.3	1106	3	US-09-583-449A-2	Sequence 2, Appl	972	126	7.0	477	3	US-08-942-562-4	Sequence 4, Appl
900	131	7.3	1106	3	US-09-435-059-2	Sequence 2, Appl	973	126	7.0	477	3	US-09-156-923-4	Sequence 4, Appl
901	131	7.3	1106	3	US-08-461-917-4	Sequence 4, Appl	974	126	7.0	822	2	US-08-359-705B-2	Sequence 2, Appl
902	131	7.3	1106	4	US-08-464-436-4	Sequence 4, Appl	975	126	7.0	822	2	US-08-286-846A-2	Sequence 2, Appl
903	131	7.3	1106	4	US-08-464-436-4	Sequence 4, Appl	976	126	7.0	822	2	US-08-457-880A-2	Sequence 2, Appl
904	131	7.3	1106	4	US-09-866-510-16	Sequence 16, Appl	977	126	7.0	822	3	US-08-942-562-2	Sequence 2, Appl
905	131	7.3	1106	4	US-09-866-510-18	Sequence 18, Appl	978	126	7.0	822	3	US-09-156-923-2	Sequence 2, Appl
906	131	7.3	1106	4	US-09-866-510-20	Sequence 20, Appl	979	126	7.0	822	3	US-09-949-016-6064	Sequence 6064, Ap
907	131	7.3	1106	4	US-09-866-510-22	Sequence 22, Appl	980	126	7.0	822	4	US-09-949-016-6064	Sequence 6064, Ap
908	131	7.3	1106	5	PCT-US92-00730-2	Sequence 2, Appl	981	126	7.0	847	1	US-08-286-305A-5	Sequence 5, Appl
909	131	7.3	1106	5	PCT-US92-00862-2	Sequence 2, Appl	982	126	7.0	847	1	US-08-441-104A-5	Sequence 5, Appl
910	130.5	7.2	298	4	US-09-152-060-76	Sequence 76, Appl	983	126	7.0	847	2	US-08-440-816A-5	Sequence 5, Appl
911	130.5	7.2	315	4	US-09-949-016-11121	Sequence 11121, A	984	126	7.0	847	3	US-09-417-381A-5	Sequence 5, Appl
912	130.5	7.2	315	4	US-09-949-016-11122	Sequence 11122, A	985	126	7.0	1000	1	US-08-222-299-2	Sequence 2, Appl
913	130.5	7.2	432	3	US-08-477-460B-2	Sequence 2, Appl	986	126	7.0	1000	2	US-08-434-878-2	Sequence 2, Appl
914	130.5	7.2	432	3	US-08-379-516-2	Sequence 2, Appl	987	126	7.0	1000	5	PCT-US95-03718-2	Sequence 2, Appl
915	130.5	7.2	432	3	US-09-329-916-2	Sequence 2, Appl	988	125.5	6.9	365	3	US-08-928-383B-2	Sequence 2, Appl
916	130.5	7.2	432	3	US-08-485-372A-2	Sequence 2, Appl	989	125.5	6.9	518	4	US-09-919-172-20	Sequence 20, Appl
917	130.5	7.2	432	3	US-09-409-006A-2	Sequence 2, Appl	990	125.5	6.9	526	4	US-09-910-174B-9	Sequence 9, Appl
918	130.5	7.2	432	4	US-08-484-681-2	Sequence 2, Appl	991	125.5	6.9	526	4	US-09-620-461-9	Sequence 9, Appl
919	130.5	7.2	432	4	US-09-766-995-2	Sequence 2, Appl	992	125.5	6.9	526	4	US-09-949-016-6122	Sequence 6122, Ap
920	130.5	7.2	432	5	PCT-US93-07422-2	Sequence 2, Appl	993	125.5	6.9	540	4	US-09-949-016-11644	Sequence 11644, A
921	130.5	7.2	466	4	US-09-604-107A-8	Sequence 8, Appl	994	125.5	6.9	589	2	US-08-724-394A-1	Sequence 1, Appl
922	130	7.2	249	4	US-09-336-536-42	Sequence 42, Appl	995	125	6.9	391	5	PCT-US95-15696-2	Sequence 2, Appl
923	130	7.2	394	4	US-09-336-536-39	Sequence 39, Appl	996	124.5	6.9	241	3	US-08-341-018-54	Sequence 54, Appl
924	130	7.2	802	3	US-09-173-151A-33	Sequence 33, Appl	997	124.5	6.9	241	3	US-08-470-335-195	Sequence 195, App
925	129.5	7.2	728	1	US-07-913-952-4	Sequence 4, Appl	998	124.5	6.9	241	3	US-08-470-339-195	Sequence 195, App
926	129	7.1	340	3	US-09-188-930-184	Sequence 184, App	999	124.5	6.9	241	3	US-08-467-602-389	Sequence 389, App
927	129	7.1	340	4	US-09-312-283C-184	Sequence 184, App	1000	124.5	6.9	241	4	US-08-470-339-195	Sequence 389, App
928	129	7.1	417	4	US-09-949-016-6729	Sequence 6729, Ap	1001	124.5	6.9	241	4	US-08-411-295F-10	Sequence 10, Appl
929	129	7.1	456	4	US-09-949-016-7564	Sequence 7564, Ap	1002	124.5	6.9	731	2	US-08-070-165F-47	Sequence 47, Appl
930	128	7.1	341	4	US-09-336-536-29	Sequence 29, Appl	1003	124	6.9	198	4	US-08-885-418-10	Sequence 10, Appl
931	128	7.1	370	4	US-09-336-536-28	Sequence 28, Appl	1004	124	6.9	198	4	US-09-569-611C-34	Sequence 34, Appl
932	128	7.1	483	2	US-08-392-338A-19	Sequence 19, Appl	1005	124	6.9	637	4	US-09-589-611C-35	Sequence 35, Appl
933	128	7.1	483	3	US-09-166-750-19	Sequence 19, Appl	1006	124	6.9	993	1	US-07-977-451-4	Sequence 4, Appl
934	128	7.1	483	3	US-09-166-093-19	Sequence 19, Appl	1007	124	6.9	993	1	US-08-252-517-4	Sequence 4, Appl
935	128	7.1	483	3	US-09-172-019-19	Sequence 19, Appl	1008	124	6.9	993	1	US-07-906-397A-4	Sequence 4, Appl
936	128	7.1	483	3	US-09-166-094-19	Sequence 19, Appl	1009	124	6.9	993	2	US-08-601-891-4	Sequence 4, Appl
937	128	7.1	483	4	US-09-443-213-19	Sequence 19, Appl	1010	124	6.9	993	2	US-09-021-324-4	Sequence 4, Appl
938	128	7.1	483	4	US-09-949-016-8574	Sequence 8574, Ap	1011	124	6.9	993	5	PCT-US92-09893-4	Sequence 4, Appl
939	128	7.1	795	4	US-09-949-016-7119	Sequence 7119, Ap	1012	124	6.9	999	1	US-08-252-626A-2	Sequence 2, Appl
940	128	7.1	806	3	US-09-383-630-3	Sequence 3, Appl	1013	124	6.9	999	4	US-09-949-016-6718	Sequence 6718, Ap
941	127.5	7.1	100	4	US-08-411-295F-121	Sequence 121, App	1014	124	6.9	1160	5	PCT-US92-05401-4	Sequence 4, Appl
942	127.5	7.1	206	3	US-08-341-018-2	Sequence 2, Appl	1015	123.5	6.8	156	4	US-08-467-602-381	Sequence 381, App
943	127.5	7.1	206	3	US-08-470-335-190	Sequence 190, App	1016	123.5	6.8	156	4	US-08-411-295F-306	Sequence 306, App
944	127.5	7.1	206	3	US-08-470-339-190	Sequence 190, App	1017	123.5	6.8	241	1	US-07-847-743B-30	Sequence 30, Appl
945	127.5	7.1	206	4	US-08-467-602-383	Sequence 383, App	1018	123.5	6.8	241	1	US-08-456-201-30	Sequence 30, Appl
946	127.5	7.1	206	4	US-08-411-295F-2	Sequence 2, Appl	1019	123.5	6.8	241	5	US-08-456-241-30	Sequence 30, Appl
947	127.5	7.1	206	4	US-08-411-295F-76	Sequence 76, Appl	1020	123.5	6.8	241	5	PCT-US92-04295A-30	Sequence 30, Appl
948	127.5	7.1	241	4	US-08-411-295F-94	Sequence 94, Appl	1021	123.5	6.8	420	1	US-07-847-743B-29	Sequence 29, Appl
949	127.5	7.1	431	3	US-09-038-832-2	Sequence 2, Appl	1022	123.5	6.8	420	1	US-08-456-201-29	Sequence 29, Appl
950	127.5	7.1	431	3	US-09-038-832-4	Sequence 4, Appl	1023	123.5	6.8	420	2	US-08-456-241-29	Sequence 29, Appl
951	127.5	7.1	447	4	US-09-949-016-8211	Sequence 8211, Ap	1024	123.5	6.8	420	5	PCT-US92-04295A-29	Sequence 29, Appl
952	127	7.0	383	4	US-09-949-016-11050	Sequence 11050, A	1025	123.5	6.8	637	1	US-07-847-743B-28	Sequence 28, Appl
953	127	7.0	992	1	US-07-813-593-2	Sequence 2, Appl	1026	123.5	6.8	637	1	US-08-456-201-28	Sequence 28, Appl
954	127	7.0	992	1	US-07-977-451-2	Sequence 2, Appl	1027	123.5	6.8	637	2	US-08-456-241-28	Sequence 28, Appl
955	127	7.0	992	1	US-07-946-507-2	Sequence 2, Appl	1028	123.5	6.8	637	5	PCT-US92-04295A-28	Sequence 28, Appl
956	127	7.0	992	1	US-08-252-517-2	Sequence 2, Appl	1029	123.5	6.8	645	1	US-07-847-743B-27	Sequence 27, Appl
957	127	7.0	992	1	US-07-906-397A-2	Sequence 2, Appl	1030	123.5	6.8	645	1	US-08-456-201-27	Sequence 27, Appl
958	127	7.0	992	1	US-08-601-891-2	Sequence 2, Appl	1031	123.5	6.8	645	1	US-08-428-926-4	Sequence 4, Appl
959	127	7.0	992	2	US-09-021-324-2	Sequence 2, Appl	1032	123.5	6.8	645	1	US-08-428-927-4	Sequence 4, Appl

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733	134.5	7.4	434	3	US-09-540-245A-19	Sequence 19, Appl	806	134.5	7.4	895	4	US-08-467-602-354	Sequence 354, App
734	134.5	7.4	456	3	US-08-470-335-246	Sequence 246, App	807	134.5	7.4	895	4	US-08-411-295F-280	Sequence 280, App
735	134.5	7.4	456	4	US-08-467-602-303	Sequence 303, App	808	134.5	7.4	898	4	US-08-467-602-351	Sequence 351, App
736	134.5	7.4	456	4	US-08-411-295F-229	Sequence 229, App	809	134.5	7.4	898	4	US-08-411-295F-277	Sequence 277, App
737	134.5	7.4	459	3	US-08-470-335-239	Sequence 239, App	810	134.5	7.4	899	3	US-08-470-335-249	Sequence 249, App
738	134.5	7.4	459	4	US-08-467-602-299	Sequence 299, App	811	134.5	7.4	899	4	US-08-467-602-301	Sequence 301, App
739	134.5	7.4	459	4	US-08-411-295F-225	Sequence 225, App	812	134.5	7.4	899	4	US-08-411-295F-227	Sequence 227, App
740	134.5	7.4	479	4	US-08-467-602-307	Sequence 307, App	813	134.5	7.4	902	3	US-08-470-335-242	Sequence 242, App
741	134.5	7.4	479	4	US-08-411-295F-233	Sequence 233, App	814	134.5	7.4	902	4	US-08-467-602-296	Sequence 296, App
742	134.5	7.4	490	4	US-08-467-602-345	Sequence 345, App	815	134.5	7.4	902	4	US-08-411-295F-222	Sequence 222, App
743	134.5	7.4	490	4	US-08-411-295F-271	Sequence 271, App	816	134.5	7.4	908	3	US-08-470-335-252	Sequence 252, App
744	134.5	7.4	493	4	US-08-467-602-341	Sequence 341, App	817	134.5	7.4	908	4	US-08-467-602-313	Sequence 313, App
745	134.5	7.4	493	4	US-08-411-295F-267	Sequence 267, App	818	134.5	7.4	908	4	US-08-411-295F-239	Sequence 239, App
746	134.5	7.4	513	4	US-08-467-602-349	Sequence 349, App	819	134.5	7.4	909	4	US-08-467-602-348	Sequence 348, App
747	134.5	7.4	513	4	US-08-411-295F-275	Sequence 275, App	820	134.5	7.4	909	4	US-08-411-295F-274	Sequence 274, App
748	134.5	7.4	526	1	US-08-471-570-4	Sequence 4, Appli	821	134.5	7.4	911	3	US-08-411-295F-245	Sequence 245, App
749	134.5	7.4	534	4	US-09-651-200-6	Sequence 6, Appli	822	134.5	7.4	911	4	US-08-470-335-245	Sequence 310, App
750	134.5	7.4	534	4	US-09-651-200-24	Sequence 24, Appl	823	134.5	7.4	911	4	US-08-467-602-310	Sequence 236, App
751	134.5	7.4	635	3	US-08-470-335-247	Sequence 247, App	824	134.5	7.4	918	4	US-08-411-295F-236	Sequence 357, App
752	134.5	7.4	635	4	US-08-467-602-302	Sequence 302, App	825	134.5	7.4	918	4	US-08-467-602-357	Sequence 357, App
753	134.5	7.4	635	4	US-08-411-295F-228	Sequence 228, App	826	134.5	7.4	922	4	US-08-411-295F-283	Sequence 283, App
754	134.5	7.4	638	3	US-08-470-335-240	Sequence 240, App	827	134.5	7.4	922	4	US-08-467-602-304	Sequence 304, App
755	134.5	7.4	638	4	US-08-467-602-297	Sequence 297, App	828	134.5	7.4	931	4	US-08-411-295F-230	Sequence 230, App
756	134.5	7.4	638	4	US-08-411-295F-223	Sequence 223, App	829	134.5	7.4	931	4	US-08-467-602-316	Sequence 316, App
757	134.5	7.4	643	5	PCr-US93-00031-19	Sequence 19, Appl	830	134.5	7.4	933	4	US-08-411-295F-242	Sequence 242, App
758	134.5	7.4	644	3	US-08-470-335-250	Sequence 250, App	831	134.5	7.4	933	4	US-08-467-602-343	Sequence 343, App
759	134.5	7.4	644	4	US-08-467-602-311	Sequence 311, App	832	134.5	7.4	936	4	US-08-411-295F-269	Sequence 269, App
760	134.5	7.4	644	4	US-08-411-295F-237	Sequence 237, App	833	134.5	7.4	936	4	US-08-467-602-338	Sequence 338, App
761	134.5	7.4	647	3	US-08-470-335-243	Sequence 243, App	834	134.5	7.4	942	4	US-08-411-295F-264	Sequence 264, App
762	134.5	7.4	647	3	US-09-009-490A-91	Sequence 91, Appli	835	134.5	7.4	942	4	US-08-467-602-355	Sequence 355, App
763	134.5	7.4	647	3	US-08-482-073-5	Sequence 5, Appli	836	134.5	7.4	945	4	US-08-411-295F-281	Sequence 281, App
764	134.5	7.4	647	4	US-08-467-602-308	Sequence 308, App	837	134.5	7.4	945	4	US-08-467-602-322	Sequence 322, App
765	134.5	7.4	647	4	US-08-411-295F-234	Sequence 234, App	838	134.5	7.4	956	4	US-08-411-295F-278	Sequence 278, App
766	134.5	7.4	647	5	PCr-US93-00031-11	Sequence 11, Appl	839	134.5	7.4	956	4	US-08-467-602-346	Sequence 346, App
767	134.5	7.4	652	1	US-08-471-570-10	Sequence 10, Appl	840	134.5	7.4	965	4	US-08-411-295F-272	Sequence 272, App
768	134.5	7.4	652	1	US-08-471-570-10	Sequence 10, Appl	841	134.5	7.4	965	4	US-08-467-602-358	Sequence 358, App
769	134.5	7.4	658	4	US-08-467-602-305	Sequence 305, App	842	134	7.4	424	6	US-08-411-295F-284	Sequence 284, App
770	134.5	7.4	658	4	US-08-411-295F-231	Sequence 231, App	843	134	7.4	424	6	5169835-6	Patent No. 5169835
771	134.5	7.4	667	4	US-08-467-602-314	Sequence 314, App	844	133.5	7.4	488	4	US-09-499-846-12	Sequence 12, Appl
772	134.5	7.4	667	4	US-08-411-295F-240	Sequence 240, App	845	133.5	7.4	888	1	US-08-445-640-35	Sequence 35, Appl
773	134.5	7.4	669	4	US-08-467-602-344	Sequence 344, App	846	133.5	7.4	888	3	US-08-170-558-35	Sequence 35, Appl
774	134.5	7.4	669	4	US-08-411-295F-270	Sequence 270, App	847	133.5	7.4	888	3	US-08-447-314-35	Sequence 35, Appl
775	134.5	7.4	672	4	US-08-467-602-339	Sequence 339, App	848	133.5	7.4	888	3	US-08-445-461-35	Sequence 35, Appl
776	134.5	7.4	672	4	US-08-411-295F-265	Sequence 265, App	849	133.5	7.4	888	4	US-09-223-490-35	Sequence 35, Appl
777	134.5	7.4	678	4	US-08-467-602-353	Sequence 353, App	850	133	7.4	317	4	US-09-684-708A-23	Sequence 23, Appl
778	134.5	7.4	678	4	US-08-411-295F-279	Sequence 279, App	851	133	7.4	322	3	US-09-383-586-33	Sequence 33, Appl
779	134.5	7.4	681	4	US-08-467-602-350	Sequence 350, App	852	133	7.4	322	4	US-09-823-038A-33	Sequence 33, Appl
780	134.5	7.4	681	4	US-08-411-295F-276	Sequence 276, App	853	133	7.4	322	4	US-09-684-708A-25	Sequence 25, Appl
781	134.5	7.4	692	4	US-08-467-602-347	Sequence 347, App	854	133	7.4	612	2	US-08-359-705B-8	Sequence 8, Appli
782	134.5	7.4	692	4	US-08-411-295F-273	Sequence 273, App	855	133	7.4	612	2	US-08-286-846A-8	Sequence 8, Appli
783	134.5	7.4	701	4	US-08-467-602-356	Sequence 356, App	856	133	7.4	612	2	US-08-457-880A-8	Sequence 8, Appli
784	134.5	7.4	701	4	US-08-411-295F-282	Sequence 282, App	857	133	7.4	612	3	US-08-444-622A-8	Sequence 8, Appli
785	134.5	7.4	740	5	PCr-US93-00031-17	Sequence 17, Appl	858	133	7.4	612	3	US-08-942-562-8	Sequence 8, Appli
786	134.5	7.4	852	3	US-08-470-335-248	Sequence 248, App	859	133	7.4	612	3	US-09-156-923-8	Sequence 8, Appli
787	134.5	7.4	852	4	US-08-467-602-300	Sequence 300, App	860	133	7.4	816	4	US-09-949-016-10904	Sequence 10904, A
788	134.5	7.4	852	4	US-08-411-295F-226	Sequence 226, App	861	133	7.4	839	2	US-08-359-705B-6	Sequence 6, Appli
789	134.5	7.4	855	3	US-08-470-335-241	Sequence 241, App	862	133	7.4	839	2	US-08-286-846A-6	Sequence 6, Appli
790	134.5	7.4	855	4	US-08-467-602-298	Sequence 298, App	863	133	7.4	839	2	US-08-457-880A-6	Sequence 6, Appli
791	134.5	7.4	855	4	US-08-411-295F-224	Sequence 224, App	864	133	7.4	839	3	US-08-444-622A-6	Sequence 6, Appli
792	134.5	7.4	861	3	US-08-470-335-251	Sequence 251, App	865	133	7.4	839	3	US-08-942-562-6	Sequence 6, Appli
793	134.5	7.4	861	4	US-08-467-602-312	Sequence 312, App	866	133	7.4	839	3	US-09-156-923-6	Sequence 6, Appli
794	134.5	7.4	861	4	US-08-411-295F-238	Sequence 238, App	867	133	7.4	850	1	US-08-286-305A-7	Sequence 7, Appli
795	134.5	7.4	864	3	US-08-470-335-244	Sequence 244, App	868	133	7.4	850	2	US-08-441-104A-7	Sequence 7, Appli
796	134.5	7.4	864	4	US-08-467-602-309	Sequence 309, App	869	133	7.4	850	2	US-08-440-816A-7	Sequence 7, Appli
797	134.5	7.4	864	4	US-08-411-295F-235	Sequence 235, App	870	133	7.4	850	3	US-09-417-381A-7	Sequence 7, Appli
798	134.5	7.4	875	4	US-08-467-602-306	Sequence 306, App	871	132	7.3	387	3	US-09-175-928-2	Sequence 2, Appli
799	134.5	7.4	875	4	US-08-411-295F-232	Sequence 232, App	872	132	7.3	408	3	US-09-724-864-62	Sequence 62, Appl
800	134.5	7.4	884	4	US-08-467-602-315	Sequence 315, App	873	131.5	7.3	312	4	US-09-254-465A-9	Sequence 9, Appli
801	134.5	7.4	884	4	US-08-411-295F-241	Sequence 241, App	883	131.5	7.3	312	4	US-09-953-499-9	Sequence 9, Appli
802	134.5	7.4	886	4	US-08-467-602-342	Sequence 342, App	884	131	7.3	240	1	US-08-471-570-12	Sequence 12, Appl
803	134.5	7.4	886	4	US-08-411-295F-268	Sequence 268, App	885	131	7.3	342	1	US-09-684-708A-27	Sequence 27, Appl
804	134.5	7.4	889	4	US-08-467-602-340	Sequence 340, App	886	131	7.3	561	4	US-09-866-510-24	Sequence 24, Appl

586	140.5	7.8	1089	3	US-09-435-059-36	Sequence 36, Appl	659	138.5	7.7	572	4	US-08-411-295F-161	Sequence 161, App
587	140.5	7.8	1089	3	US-08-461-917-2	Sequence 2, Appl	660	138.5	7.7	578	4	US-08-467-602-249	Sequence 249, App
588	140.5	7.8	1089	4	US-08-464-436-2	Sequence 2, Appl	661	138.5	7.7	578	4	US-08-411-295F-175	Sequence 175, App
589	140.5	7.8	1089	4	US-08-464-436-2	Sequence 2, Appl	662	138.5	7.7	581	4	US-08-467-602-246	Sequence 246, App
590	140.5	7.8	1089	4	US-09-769-987-2	Sequence 2, Appl	663	138.5	7.7	581	4	US-08-411-295F-172	Sequence 172, App
591	140.5	7.8	1089	4	US-09-866-510-2	Sequence 2, Appl	664	138.5	7.7	592	4	US-08-467-602-243	Sequence 243, App
592	140.5	7.8	1089	4	US-09-866-510-4	Sequence 4, Appl	665	138.5	7.7	592	4	US-08-411-295F-169	Sequence 169, App
593	140.5	7.8	1089	4	US-09-866-510-6	Sequence 6, Appl	666	138.5	7.7	601	4	US-08-467-602-252	Sequence 252, App
594	140.5	7.8	1089	4	US-09-866-510-8	Sequence 8, Appl	667	138.5	7.7	601	4	US-08-411-295F-178	Sequence 178, App
595	140.5	7.8	1089	4	US-09-866-510-10	Sequence 10, Appl	668	138.5	7.7	603	4	US-08-467-602-279	Sequence 279, App
596	140.5	7.8	1089	4	US-09-919-497-90	Sequence 90, Appl	669	138.5	7.7	603	4	US-08-411-295F-205	Sequence 205, App
597	140.5	7.8	1089	4	US-09-949-016-6703	Sequence 90, Appl	670	138.5	7.7	606	4	US-08-467-602-277	Sequence 277, App
598	140.5	7.8	1089	5	PCT-US92-00730-4	Sequence 4, Appl	671	138.5	7.7	606	4	US-08-411-295F-203	Sequence 203, App
599	140.5	7.8	1089	5	PCT-US92-00862-4	Sequence 4, Appl	672	138.5	7.7	612	4	US-08-467-602-291	Sequence 291, App
600	140	7.8	203	4	US-09-270-767-60345	Sequence 60345, A	673	138.5	7.7	612	4	US-08-411-295F-217	Sequence 217, App
601	140	7.8	801	3	US-09-383-630-6	Sequence 6, Appl	674	138.5	7.7	615	4	US-08-467-602-288	Sequence 288, App
602	140	7.8	890	1	US-08-445-640-2	Sequence 2, Appl	675	138.5	7.7	615	4	US-08-411-295F-214	Sequence 214, App
603	140	7.8	890	3	US-08-170-558-2	Sequence 2, Appl	676	138.5	7.7	616	4	US-08-467-602-238	Sequence 238, App
604	140	7.8	890	3	US-08-447-314-2	Sequence 2, Appl	677	138.5	7.7	616	4	US-08-411-295F-164	Sequence 164, App
605	140	7.8	890	3	US-08-445-461-2	Sequence 2, Appl	678	138.5	7.7	619	4	US-08-467-602-233	Sequence 233, App
606	140	7.8	890	4	US-09-223-490-2	Sequence 2, Appl	679	138.5	7.7	619	4	US-08-411-295F-159	Sequence 159, App
607	140	7.8	911	1	US-08-286-305A-1	Sequence 1, Appl	680	138.5	7.7	625	4	US-08-467-602-250	Sequence 250, App
608	140	7.8	911	2	US-08-441-104A-1	Sequence 1, Appl	681	138.5	7.7	625	4	US-08-411-295F-176	Sequence 176, App
609	140	7.8	911	2	US-08-440-816A-1	Sequence 1, Appl	682	138.5	7.7	626	4	US-08-467-602-285	Sequence 285, App
610	140	7.8	911	3	US-09-417-381A-1	Sequence 1, Appl	683	138.5	7.7	626	4	US-08-411-295F-211	Sequence 211, App
611	140	7.8	976	3	US-08-750-141A-1	Sequence 1, Appl	684	138.5	7.7	628	4	US-08-467-602-247	Sequence 247, App
612	139.5	7.7	263	3	US-08-341-018-4	Sequence 4, Appl	685	138.5	7.7	628	4	US-08-411-295F-173	Sequence 173, App
613	139.5	7.7	263	3	US-08-470-335-191	Sequence 191, App	686	138.5	7.7	635	4	US-08-467-602-294	Sequence 294, App
614	139.5	7.7	263	3	US-08-470-339-191	Sequence 191, App	687	138.5	7.7	635	4	US-08-411-295F-220	Sequence 220, App
615	139.5	7.7	263	4	US-08-467-602-385	Sequence 191, App	688	138.5	7.7	639	4	US-08-467-602-241	Sequence 241, App
616	139.5	7.7	419	6	5169835-2	Sequence 185, App	689	138.5	7.7	639	4	US-08-411-295F-167	Sequence 167, App
617	139.5	7.7	419	6	5169835-2	Patent No. 5169835	690	138.5	7.7	648	4	US-08-467-602-253	Sequence 253, App
618	139	7.7	272	1	US-08-282-951-6	Sequence 6, Appl	691	138.5	7.7	648	4	US-08-411-295F-179	Sequence 179, App
619	138.5	7.7	173	4	US-08-986-485-4	Sequence 4, Appl	692	138.5	7.7	650	4	US-08-467-602-280	Sequence 280, App
620	138.5	7.7	173	4	US-08-467-602-240	Sequence 240, App	693	138.5	7.7	650	4	US-08-411-295F-206	Sequence 206, App
621	138.5	7.7	176	4	US-08-411-295F-166	Sequence 166, App	694	138.5	7.7	653	4	US-08-467-602-275	Sequence 275, App
622	138.5	7.7	176	4	US-08-467-602-236	Sequence 236, App	695	138.5	7.7	653	4	US-08-411-295F-201	Sequence 201, App
623	138.5	7.7	176	4	US-08-411-295F-162	Sequence 162, App	696	138.5	7.7	659	4	US-08-467-602-292	Sequence 292, App
624	138.5	7.7	196	4	US-08-467-602-244	Sequence 244, App	697	138.5	7.7	659	4	US-08-411-295F-218	Sequence 218, App
625	138.5	7.7	196	4	US-08-411-295F-170	Sequence 170, App	698	138.5	7.7	662	4	US-08-467-602-289	Sequence 289, App
626	138.5	7.7	207	4	US-08-467-602-282	Sequence 282, App	699	138.5	7.7	662	4	US-08-411-295F-215	Sequence 215, App
627	138.5	7.7	207	4	US-08-411-295F-208	Sequence 208, App	700	138.5	7.7	673	4	US-08-467-602-283	Sequence 283, App
628	138.5	7.7	210	4	US-08-467-602-278	Sequence 278, App	701	138.5	7.7	673	4	US-08-411-295F-209	Sequence 209, App
629	138.5	7.7	210	4	US-08-411-295F-204	Sequence 204, App	702	138.5	7.7	682	4	US-08-467-602-295	Sequence 295, App
630	138.5	7.7	230	4	US-08-467-602-286	Sequence 286, App	703	138.5	7.7	682	4	US-08-411-295F-221	Sequence 221, App
631	138.5	7.7	230	4	US-08-411-295F-212	Sequence 212, App	704	137	7.6	514	4	US-08-949-016-11380	Sequence 11380, A
632	138.5	7.7	352	4	US-08-467-602-239	Sequence 239, App	705	137	7.6	517	4	US-09-723-368-4	Sequence 4, Appl
633	138.5	7.7	352	4	US-08-411-295F-165	Sequence 165, App	706	136.5	7.6	388	1	US-08-445-640-6	Sequence 6, Appl
634	138.5	7.7	355	4	US-08-467-602-234	Sequence 234, App	707	136.5	7.6	388	3	US-08-170-558-6	Sequence 6, Appl
635	138.5	7.7	355	4	US-08-411-295F-160	Sequence 160, App	708	136.5	7.6	388	3	US-08-447-314-6	Sequence 6, Appl
636	138.5	7.7	361	4	US-08-467-602-248	Sequence 248, App	709	136.5	7.6	388	3	US-08-445-461-6	Sequence 6, Appl
637	138.5	7.7	361	4	US-08-411-295F-174	Sequence 174, App	710	136.5	7.6	388	4	US-09-223-490-6	Sequence 6, Appl
638	138.5	7.7	364	4	US-08-467-602-245	Sequence 245, App	711	136.5	7.6	498	4	US-09-354-151-2	Sequence 32, Appl
639	138.5	7.7	364	4	US-08-411-295F-171	Sequence 171, App	712	136.5	7.6	498	3	US-08-478-208-32	Sequence 32, Appl
640	138.5	7.7	375	4	US-08-467-602-242	Sequence 242, App	713	136.5	7.6	738	4	US-09-336-536-73	Sequence 73, Appl
641	138.5	7.7	375	4	US-08-411-295F-168	Sequence 168, App	714	136.5	7.6	738	6	5264554-2	Patent No. 5264554
642	138.5	7.7	384	4	US-08-467-602-251	Sequence 251, App	715	136.5	7.6	738	6	5264554-2	Patent No. 5264554
643	138.5	7.7	384	4	US-08-411-295F-177	Sequence 177, App	716	136	7.5	393	1	US-08-429-742-2	Sequence 2, Appl
644	138.5	7.7	386	4	US-08-467-602-281	Sequence 281, App	717	136	7.5	458	4	US-09-435-956A-1	Sequence 1, Appl
645	138.5	7.7	386	4	US-08-411-295F-207	Sequence 207, App	718	136	7.5	458	4	PCT-US93-00031-21	Sequence 21, Appl
646	138.5	7.7	389	4	US-08-467-602-276	Sequence 276, App	719	135.5	7.5	371	4	US-08-411-295F-308	Sequence 308, App
647	138.5	7.7	389	4	US-08-411-295F-202	Sequence 202, App	720	135.5	7.5	405	4	US-08-467-602-384	Sequence 384, App
648	138.5	7.7	395	4	US-08-467-602-290	Sequence 290, App	721	135.5	7.5	405	4	US-08-411-295F-307	Sequence 307, App
649	138.5	7.7	395	4	US-08-411-295F-216	Sequence 216, App	722	135.5	7.5	501	3	US-08-891-845-10	Sequence 10, Appl
650	138.5	7.7	398	4	US-08-467-602-287	Sequence 287, App	723	135.5	7.5	501	3	US-09-514-573-10	Sequence 10, Appl
651	138.5	7.7	398	4	US-08-411-295F-213	Sequence 213, App	724	135.5	7.5	768	3	US-08-891-845-2	Sequence 2, Appl
652	138.5	7.7	409	4	US-08-467-602-284	Sequence 284, App	725	135.5	7.5	768	4	US-09-514-573-2	Sequence 2, Appl
653	138.5	7.7	409	4	US-08-411-295F-210	Sequence 210, App	726	135	7.5	492	3	US-08-462-794-11	Sequence 11, Appl
654	138.5	7.7	418	4	US-08-467-602-293	Sequence 293, App	727	135	7.5	497	4	US-09-499-846-6	Sequence 6, Appl
655	138.5	7.7	418	4	US-08-411-295F-219	Sequence 219, App	728	135	7.5	497	4	US-09-499-846-10	Sequence 10, Appl
656	138.5	7.7	569	4	US-08-467-602-237	Sequence 237, App	729	135	7.5	525	4	US-09-499-846-4	Sequence 4, Appl
657	138.5	7.7	569	4	US-08-411-295F-163	Sequence 163, App	730	135	7.5	525	4	US-09-499-846-8	Sequence 8, Appl
658	138.5	7.7	572	4	US-08-467-602-235	Sequence 235, App	731	134.5	7.4	349	3	US-08-470-335-188	Sequence 188, App

440	150.5	8.3	841	4	US-08-411-295F-253	Sequence 253, App	513	147.5	8.2	403	4	US-09-638-648-5	Sequence 5, Appli
441	150.5	8.3	850	4	US-08-467-602-336	Sequence 336, App	514	145.5	8.1	252	4	US-09-270-767-44627	Sequence 44627, A
442	150.5	8.3	850	4	US-08-411-295F-262	Sequence 262, App	515	145.5	8.1	549	4	US-09-858-664A-5	Sequence 5, Appli
443	150.5	8.3	852	4	US-08-467-602-363	Sequence 363, App	516	145.5	8.1	549	4	US-10-274-978-6	Sequence 6, Appli
444	150.5	8.3	852	4	US-08-411-295F-289	Sequence 289, App	517	145.5	8.1	549	4	US-10-697-263-6	Sequence 6, Appli
445	150.5	8.3	855	4	US-08-467-602-361	Sequence 361, App	518	145	8.0	972	3	US-08-750-141A-2	Sequence 20, Appli
446	150.5	8.3	855	4	US-08-411-295F-287	Sequence 287, App	519	145	8.0	972	4	US-09-544-807-10	Sequence 10, Appli
447	150.5	8.3	861	4	US-08-467-602-375	Sequence 375, App	520	144	8.0	891	4	US-09-345-473B-25	Sequence 25, Appli
448	150.5	8.3	861	4	US-08-411-295F-301	Sequence 301, App	521	143.5	7.9	344	2	US-08-602-725-34	Sequence 34, Appli
449	150.5	8.3	864	4	US-08-467-602-372	Sequence 372, App	522	143.5	7.9	662	1	US-08-261-304-7	Sequence 7, Appli
450	150.5	8.3	864	4	US-08-411-295F-298	Sequence 298, App	523	143	7.9	661	1	US-08-233-538-12	Sequence 12, Appli
451	150.5	8.3	865	4	US-08-470-335-235	Sequence 235, App	524	143	7.9	661	2	US-08-786-164-12	Sequence 12, Appli
452	150.5	8.3	865	4	US-08-467-602-322	Sequence 322, App	525	143	7.9	687	1	US-08-232-538-6	Sequence 6, Appli
453	150.5	8.3	865	4	US-08-411-295F-248	Sequence 248, App	526	143	7.9	687	2	US-08-786-164-6	Sequence 6, Appli
454	150.5	8.3	868	3	US-08-470-335-229	Sequence 229, App	527	143	7.9	687	3	US-09-427-353-2	Sequence 2, Appli
455	150.5	8.3	868	4	US-08-467-602-317	Sequence 317, App	528	142.5	7.9	263	4	US-09-592-998F-77	Sequence 77, Appli
456	150.5	8.3	868	4	US-08-411-295F-243	Sequence 243, App	529	142.5	7.9	431	4	US-09-592-998C-9	Sequence 9, Appli
457	150.5	8.3	874	3	US-08-470-335-238	Sequence 238, App	530	142.5	7.9	435	4	US-09-592-998C-10	Sequence 10, Appli
458	150.5	8.3	874	4	US-08-467-602-334	Sequence 334, App	531	142.5	7.9	735	5	PCT-US93-00031-13	Sequence 13, Appli
459	150.5	8.3	874	4	US-08-411-295F-260	Sequence 260, App	532	142.5	7.9	739	3	US-08-483-073-6	Sequence 6, Appli
460	150.5	8.3	875	4	US-08-467-602-369	Sequence 369, App	533	142.5	7.9	739	5	PCT-US93-00031-9	Sequence 9, Appli
461	150.5	8.3	875	4	US-08-411-295F-295	Sequence 295, App	534	141.5	7.8	254	3	US-08-470-335-193	Sequence 193, Appli
462	150.5	8.3	877	3	US-08-470-335-232	Sequence 232, App	535	141.5	7.8	257	3	US-08-341-018-6	Sequence 6, Appli
463	150.5	8.3	877	4	US-08-467-602-331	Sequence 331, App	536	141.5	7.8	257	3	US-08-470-339-193	Sequence 193, Appli
464	150.5	8.3	877	4	US-08-411-295F-257	Sequence 257, App	537	141.5	7.8	257	4	US-08-467-602-387	Sequence 387, Appli
465	150.5	8.3	884	4	US-08-467-602-378	Sequence 378, App	538	141.5	7.8	257	4	US-08-411-295F-6	Sequence 6, Appli
466	150.5	8.3	884	4	US-08-411-295F-304	Sequence 304, App	539	141.5	7.8	263	4	US-08-411-295F-4	Sequence 4, Appli
467	150.5	8.3	888	4	US-08-467-602-325	Sequence 325, App	540	141.5	7.8	280	3	US-08-341-018-56	Sequence 56, Appli
468	150.5	8.3	888	4	US-08-411-295F-251	Sequence 251, App	541	141.5	7.8	280	3	US-08-470-335-192	Sequence 192, Appli
469	150.5	8.3	897	4	US-08-467-602-337	Sequence 337, App	542	141.5	7.8	280	3	US-08-470-339-192	Sequence 192, Appli
470	150.5	8.3	897	4	US-08-411-295F-263	Sequence 263, App	543	141.5	7.8	280	4	US-08-467-602-386	Sequence 386, Appli
471	150.5	8.3	899	4	US-08-467-602-364	Sequence 364, App	544	141.5	7.8	280	4	US-08-411-295F-95	Sequence 95, Appli
472	150.5	8.3	899	4	US-08-411-295F-290	Sequence 290, App	545	141.5	7.8	280	4	US-08-411-295F-95	Sequence 95, Appli
473	150.5	8.3	902	4	US-08-467-602-359	Sequence 359, App	546	141.5	7.8	388	1	US-08-445-640-12	Sequence 12, Appli
474	150.5	8.3	902	4	US-08-411-295F-285	Sequence 285, App	547	141.5	7.8	388	3	US-08-170-558-12	Sequence 12, Appli
475	150.5	8.3	908	4	US-08-467-602-376	Sequence 376, App	548	141.5	7.8	388	3	US-08-447-314-12	Sequence 12, Appli
476	150.5	8.3	908	4	US-08-411-295F-302	Sequence 302, App	549	141.5	7.8	388	3	US-08-445-461-12	Sequence 12, Appli
477	150.5	8.3	911	4	US-08-467-602-373	Sequence 373, App	550	141.5	7.8	388	4	US-09-223-490-12	Sequence 12, Appli
478	150.5	8.3	911	4	US-08-411-295F-299	Sequence 299, App	551	141	7.8	471	4	US-09-949-016-9042	Sequence 9042, Ap
479	150.5	8.3	922	4	US-08-467-602-367	Sequence 367, App	552	141	7.8	471	4	US-09-949-016-9043	Sequence 9043, Ap
480	150.5	8.3	922	4	US-08-411-295F-293	Sequence 293, App	553	141	7.8	471	4	US-09-949-016-9044	Sequence 9044, Ap
481	150.5	8.3	931	4	US-08-467-602-379	Sequence 379, App	554	141	7.8	471	4	US-09-949-016-9045	Sequence 9045, Ap
482	150.5	8.3	931	4	US-08-411-295F-305	Sequence 305, App	555	141	7.8	471	4	US-09-949-016-9046	Sequence 9046, Ap
483	150.5	8.3	1298	1	US-08-222-616-33	Sequence 33, Appli	556	141	7.8	471	4	US-09-949-016-9047	Sequence 9047, Ap
484	150.5	8.3	1298	1	US-08-340-011-2	Sequence 2, Appli	557	141	7.8	471	4	US-09-949-016-9048	Sequence 9048, Ap
485	150.5	8.3	1298	3	US-08-901-710-2	Sequence 2, Appli	558	141	7.8	471	4	US-09-949-016-9049	Sequence 9049, Ap
486	150.5	8.3	1298	3	US-08-446-648-33	Sequence 33, Appli	559	141	7.8	471	4	US-09-949-016-9050	Sequence 9050, Ap
487	150.5	8.3	1298	4	US-09-982-610-33	Sequence 33, Appli	560	141	7.8	471	4	US-09-949-016-9051	Sequence 9051, Ap
488	150.5	8.3	1298	4	US-09-169-079-2	Sequence 2, Appli	561	141	7.8	821	2	US-08-451-822A-13	Sequence 13, Appli
489	150.5	8.3	1298	5	PCT-US95-04228-33	Sequence 33, Appli	562	141	7.8	821	3	US-08-323-430-13	Sequence 13, Appli
490	150.5	8.3	1362	2	US-08-874-678-33	Sequence 33, Appli	563	140.5	7.8	257	4	US-08-411-295F-78	Sequence 78, Appli
491	150.5	8.3	1362	3	US-08-643-839-33	Sequence 33, Appli	564	140.5	7.8	552	4	US-09-969-532-8	Sequence 8, Appli
492	150.5	8.3	1362	3	US-09-348-886-33	Sequence 33, Appli	565	140.5	7.8	563	4	US-09-969-532-6	Sequence 6, Appli
493	150.5	8.3	1363	1	US-08-340-011-4	Sequence 4, Appli	566	140.5	7.8	566	4	US-09-969-532-4	Sequence 4, Appli
494	150.5	8.3	1363	3	US-08-901-710-4	Sequence 4, Appli	567	140.5	7.8	577	4	US-09-969-532-2	Sequence 2, Appli
495	150.5	8.3	1363	4	US-09-375-248-2	Sequence 2, Appli	568	140.5	7.8	589	4	US-09-866-510-12	Sequence 12, Appli
496	150.5	8.3	1363	4	US-09-169-079-4	Sequence 4, Appli	569	140.5	7.8	762	4	US-09-949-016-7568	Sequence 7568, Ap
497	150.5	8.3	1368	2	US-08-874-678-34	Sequence 34, Appli	570	140.5	7.8	886	4	US-09-969-532-16	Sequence 16, Appli
498	150.5	8.3	1368	3	US-08-643-839-34	Sequence 34, Appli	571	140.5	7.8	897	4	US-09-969-532-14	Sequence 14, Appli
499	150.5	8.3	1368	3	US-09-348-886-34	Sequence 34, Appli	572	140.5	7.8	900	4	US-09-969-532-12	Sequence 12, Appli
500	150	8.3	355	1	US-08-471-570-14	Sequence 14, Appli	573	140.5	7.8	911	4	US-09-969-532-10	Sequence 10, Appli
501	150	8.3	643	1	US-08-471-570-6	Sequence 6, Appli	574	140.5	7.8	1088	4	US-09-961-403-4	Sequence 4, Appli
502	150	8.3	769	1	US-08-447-464-3	Sequence 3, Appli	575	140.5	7.8	1089	1	US-08-180-195-36	Sequence 36, Appli
503	149.5	8.3	1501	2	US-08-716-679-3	Sequence 3, Appli	576	140.5	7.8	1089	1	US-08-168-917-4	Sequence 4, Appli
504	149.5	8.3	1501	2	US-08-429-742-4	Sequence 4, Appli	577	140.5	7.8	1089	2	US-08-477-329-36	Sequence 36, Appli
505	149	8.3	388	1	US-08-429-742-4	Sequence 4, Appli	578	140.5	7.8	1089	2	US-08-475-458-36	Sequence 36, Appli
506	148.5	8.2	1911	1	US-08-348-006B-5	Sequence 5, Appli	579	140.5	7.8	1089	2	US-08-460-510-4	Sequence 4, Appli
507	148.5	8.2	1911	2	US-08-800-825A-5	Sequence 5, Appli	580	140.5	7.8	1089	2	US-08-460-490-4	Sequence 4, Appli
508	148.5	8.2	1911	3	US-09-158-657-5	Sequence 5, Appli	581	140.5	7.8	1089	3	US-08-980-400-36	Sequence 36, Appli
509	148.5	8.2	1911	5	PCT-US94-10166-5	Sequence 5, Appli	582	140.5	7.8	1089	3	US-08-462-728-2	Sequence 2, Appli
510	148	8.2	602	1	US-08-168-091A-2	Sequence 2, Appli	583	140.5	7.8	1089	3	US-09-583-459A-36	Sequence 36, Appli
511	148	8.2	820	1	US-08-166-717D-6	Sequence 6, Appli	584	140.5	7.8	1089	3	US-09-583-210-35	Sequence 35, Appli
512	147.5	8.2	403	4	US-09-638-649-5	Sequence 5, Appli	585	140.5	7.8	1089	3	US-09-583-449A-36	Sequence 36, Appli

285	157	8.7	263	4	US-09-953-499-25	Sequence 25, Appl	367	151.5	8.4	422	4	US-08-467-602-170	Sequence 170, App
286	157	8.7	299	3	US-09-188-930-331	Sequence 331, Appl	368	151.5	8.4	422	4	US-08-411-295F-65	Sequence 65, Appl
287	157	8.7	299	3	US-09-462-270-2	Sequence 2, Appl	369	151.5	8.4	422	4	US-08-411-295F-66	Sequence 66, Appl
288	157	8.7	299	4	US-09-254-465A-1	Sequence 1, Appl	370	151.5	8.4	422	4	US-08-411-295F-69	Sequence 69, Appl
289	157	8.7	299	4	US-09-312-283C-189	Sequence 189, Appl	371	151.5	8.4	422	4	US-08-411-295F-103	Sequence 103, Appl
290	157	8.7	299	4	US-09-312-283C-331	Sequence 331, Appl	372	151.5	8.4	422	5	PCT-US94-05083C-166	Sequence 166, App
294	157	8.7	299	4	US-09-397-243D-3	Sequence 3, Appl	373	151.5	8.4	422	5	PCT-US95-06846A-170	Sequence 170, App
301	157	8.7	299	4	US-09-953-499-1	Sequence 1, Appl	374	151.5	8.4	422	5	PCT-US95-06846A-170	Sequence 32, Appl
302	156.5	8.7	416	4	US-09-638-649-1	Sequence 1, Appl	375	151.5	8.4	1363	2	US-08-874-678-32	Sequence 32, Appl
303	156.5	8.7	416	4	US-08-755-235-2	Sequence 2, Appl	376	151.5	8.4	1363	3	US-08-643-839-32	Sequence 32, Appl
304	156.5	8.7	416	4	US-09-638-648-1	Sequence 1, Appl	377	151.5	8.4	1363	3	US-09-348-886-32	Sequence 32, Appl
305	155.5	8.6	299	3	US-09-188-930-189	Sequence 189, App	378	151	8.4	874	2	US-08-456-647B-6	Sequence 6, Appl
306	155.5	8.6	880	1	US-08-445-640-10	Sequence 10, Appl	379	151	8.4	874	2	US-08-237-401A-6	Sequence 6, Appl
307	155.5	8.6	880	3	US-08-170-558-10	Sequence 10, Appl	380	150.5	8.3	349	4	US-08-924-103-4	Sequence 4, Appl
308	155.5	8.6	880	3	US-08-447-314-10	Sequence 10, Appl	381	150.5	8.3	411	3	US-08-470-339-189	Sequence 189, App
309	155.5	8.6	880	3	US-08-445-461-10	Sequence 10, Appl	382	150.5	8.3	414	3	US-08-470-339-188	Sequence 188, App
310	155.5	8.6	880	4	US-09-223-490-10	Sequence 10, Appl	383	150.5	8.3	422	4	US-08-467-602-324	Sequence 324, App
311	155	8.6	805	3	US-08-985-526-34	Sequence 34, Appl	384	150.5	8.3	422	4	US-08-411-295F-250	Sequence 250, App
312	155	8.6	1248	4	US-09-949-016-10595	Sequence 10595, A	385	150.5	8.3	425	3	US-08-470-335-226	Sequence 226, App
313	155	8.6	1248	4	US-09-949-016-10596	Sequence 10596, A	386	150.5	8.3	425	4	US-08-467-602-320	Sequence 320, App
314	155	8.6	1363	4	US-09-375-248-19	Sequence 19, Appl	387	150.5	8.3	425	4	US-08-411-295F-246	Sequence 246, App
315	155	8.6	1367	1	US-07-813-593-4	Sequence 4, Appl	388	150.5	8.3	445	4	US-08-467-602-328	Sequence 328, App
316	155	8.6	1367	1	US-07-977-451-6	Sequence 6, Appl	389	150.5	8.3	445	4	US-08-411-295F-254	Sequence 254, App
317	155	8.6	1367	1	US-07-946-507-4	Sequence 4, Appl	390	150.5	8.3	456	4	US-08-467-602-366	Sequence 366, App
318	155	8.6	1367	1	US-08-252-517-6	Sequence 6, Appl	391	150.5	8.3	456	4	US-08-411-295F-292	Sequence 292, App
319	155	8.6	1367	1	US-07-906-397A-6	Sequence 6, Appl	392	150.5	8.3	459	4	US-08-467-602-362	Sequence 362, App
320	155	8.6	1367	1	US-08-601-891-6	Sequence 6, Appl	393	150.5	8.3	459	4	US-08-411-295F-288	Sequence 288, App
321	155	8.6	1367	2	US-09-021-324-6	Sequence 6, Appl	394	150.5	8.3	479	4	US-08-467-602-370	Sequence 370, App
322	155	8.6	1367	4	US-09-872-136B-6	Sequence 6, Appl	395	150.5	8.3	479	4	US-08-411-295F-296	Sequence 296, App
323	155	8.6	1367	5	PCT-US92-02750-8	Sequence 8, Appl	396	150.5	8.3	601	3	US-08-470-335-233	Sequence 233, App
324	155	8.6	1367	5	PCT-US92-05401-6	Sequence 6, Appl	397	150.5	8.3	601	4	US-08-467-602-323	Sequence 323, App
325	155	8.6	1367	5	PCT-US92-09893-6	Sequence 6, Appl	398	150.5	8.3	601	4	US-08-411-295F-249	Sequence 249, App
326	154.5	8.6	462	2	US-08-752-307B-7	Sequence 7, Appl	399	150.5	8.3	604	3	US-08-470-335-227	Sequence 227, App
327	154.5	8.6	462	3	US-09-707-802-7	Sequence 7, Appl	400	150.5	8.3	604	4	US-08-467-602-318	Sequence 318, App
328	154.5	8.6	462	3	US-09-991-326-7	Sequence 7, Appl	401	150.5	8.3	604	4	US-08-411-295F-244	Sequence 244, App
329	154.5	8.6	465	2	US-08-752-307B-5	Sequence 5, Appl	402	150.5	8.3	610	3	US-08-470-335-236	Sequence 236, App
330	154.5	8.6	465	3	US-09-707-802-5	Sequence 5, Appl	403	150.5	8.3	610	4	US-08-467-602-332	Sequence 332, App
331	154.5	8.6	465	3	US-09-991-326-5	Sequence 5, Appl	404	150.5	8.3	610	4	US-08-411-295F-258	Sequence 258, App
332	154.5	8.6	602	1	US-08-428-926-5	Sequence 5, Appl	405	150.5	8.3	613	3	US-08-470-335-230	Sequence 230, App
333	154.5	8.6	602	1	US-08-428-927-5	Sequence 5, Appl	406	150.5	8.3	613	4	US-08-467-602-329	Sequence 329, App
334	154.5	8.6	602	1	US-08-428-298-5	Sequence 5, Appl	407	150.5	8.3	613	4	US-08-411-295F-255	Sequence 255, App
335	154.5	8.6	602	1	US-08-339-517-5	Sequence 5, Appl	408	150.5	8.3	624	4	US-08-467-602-326	Sequence 326, App
336	154.5	8.6	1311	1	US-08-340-011-5	Sequence 5, Appl	409	150.5	8.3	624	4	US-08-411-295F-252	Sequence 252, App
337	154.5	8.6	1311	3	US-08-901-710-5	Sequence 5, Appl	410	150.5	8.3	633	4	US-08-467-602-335	Sequence 335, App
338	154.5	8.6	1311	4	US-09-169-079-5	Sequence 5, Appl	411	150.5	8.3	633	4	US-08-411-295F-261	Sequence 261, App
339	154	8.5	579	3	US-09-173-151A-2	Sequence 2, Appl	412	150.5	8.3	635	4	US-08-467-602-365	Sequence 365, App
340	154	8.5	686	3	US-09-173-151A-4	Sequence 4, Appl	413	150.5	8.3	635	4	US-08-411-295F-291	Sequence 291, App
341	153.5	8.5	477	2	US-08-432-016-3	Sequence 3, Appl	414	150.5	8.3	638	4	US-08-467-602-360	Sequence 360, App
342	153.5	8.5	477	2	US-08-684-594-3	Sequence 3, Appl	415	150.5	8.3	638	4	US-08-411-295F-286	Sequence 286, App
343	153	8.5	189	4	US-09-270-767-32726	Sequence 32726, A	416	150.5	8.3	644	4	US-08-467-602-374	Sequence 374, App
344	153	8.5	189	4	US-09-270-767-47943	Sequence 47943, A	417	150.5	8.3	644	4	US-08-411-295F-300	Sequence 300, App
345	153	8.5	524	4	US-09-270-767-44009	Sequence 44009, A	418	150.5	8.3	647	4	US-08-467-602-371	Sequence 371, App
346	153	8.5	894	4	US-09-949-016-10605	Sequence 10605, A	419	150.5	8.3	647	4	US-08-411-295F-297	Sequence 297, App
347	152	8.4	351	5	PCT-US93-05703-2	Sequence 2, Appl	420	150.5	8.3	658	4	US-08-467-602-368	Sequence 368, App
348	152	8.4	1123	4	US-09-949-016-6230	Sequence 6230, Ap	421	150.5	8.3	658	4	US-08-411-295F-294	Sequence 294, App
349	152	8.4	1128	4	US-09-949-016-7522	Sequence 7522, Ap	422	150.5	8.3	667	4	US-08-467-602-377	Sequence 377, App
350	151.5	8.4	227	4	US-09-205-258-947	Sequence 947, App	423	150.5	8.3	667	4	US-08-411-295F-303	Sequence 303, App
351	151.5	8.4	365	4	US-09-949-016-7591	Sequence 7591, Ap	424	150.5	8.3	777	2	US-08-874-678-3	Sequence 3, Appl
352	151.5	8.4	422	1	US-08-036-555B-170	Sequence 170, App	425	150.5	8.3	777	3	US-08-643-839-3	Sequence 3, Appl
353	151.5	8.4	422	1	US-08-469-569-170	Sequence 170, App	426	150.5	8.3	777	3	US-09-348-886-3	Sequence 3, Appl
354	151.5	8.4	422	1	US-08-428-926-3	Sequence 3, Appl	427	150.5	8.3	818	3	US-08-470-335-234	Sequence 234, App
355	151.5	8.4	422	1	US-08-428-927-3	Sequence 3, Appl	428	150.5	8.3	818	4	US-08-467-602-321	Sequence 321, App
356	151.5	8.4	422	1	US-08-428-927-3	Sequence 3, Appl	429	150.5	8.3	821	4	US-08-411-295F-247	Sequence 247, App
357	151.5	8.4	422	1	US-08-428-298-3	Sequence 3, Appl	430	150.5	8.3	821	3	US-08-470-335-228	Sequence 228, App
358	151.5	8.4	422	1	US-08-339-517-3	Sequence 3, Appl	431	150.5	8.3	821	4	US-08-467-602-319	Sequence 319, App
359	151.5	8.4	422	1	US-08-469-526A-170	Sequence 170, App	432	150.5	8.3	821	4	US-08-411-295F-245	Sequence 245, App
360	151.5	8.4	422	2	US-08-734-591A-170	Sequence 170, App	433	150.5	8.3	827	3	US-08-470-335-237	Sequence 237, App
361	151.5	8.4	422	2	US-08-469-660-170	Sequence 170, App	434	150.5	8.3	827	3	US-08-467-602-333	Sequence 333, App
362	151.5	8.4	422	3	US-08-341-018-72	Sequence 72, Appl	435	150.5	8.3	827	4	US-08-411-295F-259	Sequence 259, App
363	151.5	8.4	422	3	US-08-470-335-170	Sequence 170, App	436	150.5	8.3	830	3	US-08-470-335-231	Sequence 231, App
364	151.5	8.4	422	3	US-08-735-021-170	Sequence 170, App	437	150.5	8.3	830	4	US-08-467-602-330	Sequence 330, App
365	151.5	8.4	422	3	US-08-734-664A-170	Sequence 170, App	438	150.5	8.3	841	4	US-08-411-295F-256	Sequence 256, App
366	151.5	8.4	422	3	US-08-470-339-170	Sequence 170, App	439	150.5	8.3	841	4	US-08-467-602-327	Sequence 327, App

130	192.5	10.7	1150	4	US-09-877-730-8	Sequence 8, Appli	203	165.5	9.2	583	2	US-08-432-016-2	Sequence 2, Appli
131	192.5	10.7	1260	3	US-08-506-296B-21	Sequence 28, Appl	204	165.5	9.2	583	2	US-08-684-594-2	Sequence 2, Appli
132	192.5	10.7	1268	3	US-08-506-296B-28	Sequence 21, Appl	205	165.5	9.2	646	4	US-09-949-016-6728	Sequence 6728, Ap
133	192	10.6	529	3	US-09-383-585-31	Sequence 31, Appl	206	165.5	9.2	646	4	US-09-653-961-4	Sequence 4, Appli
134	192	10.6	529	3	US-09-823-038A-31	Sequence 31, Appl	207	165.5	9.2	828	1	US-08-261-304-2	Sequence 2, Appli
135	191.5	10.6	1209	4	US-09-130-158A-2	Sequence 2, Appli	208	165.5	9.2	1617	4	US-09-784-358-16	Sequence 16, Appl
136	188.5	10.4	651	4	US-09-270-767-44877	Sequence 44877, A	209	165.5	9.2	1691	4	US-09-784-358-2	Sequence 2, Appli
137	187.5	10.4	1266	3	US-08-506-296B-4	Sequence 4, Appli	210	165	9.1	501	2	US-08-408-095-31	Sequence 31, Appl
138	185.5	10.3	318	2	US-08-633-148-4	Sequence 4, Appli	211	164	9.1	439	3	US-09-383-586-32	Sequence 32, Appl
139	185.5	10.3	332	4	US-09-062-365-1	Sequence 1, Appli	212	164	9.1	439	3	US-09-823-038A-32	Sequence 32, Appl
140	185.5	10.3	340	2	US-08-633-148-2	Sequence 2, Appli	213	164	9.1	640	4	US-09-949-016-7565	Sequence 7565, Ap
141	185.5	10.3	404	4	US-09-949-016-11025	Sequence 11025, A	214	163.5	9.1	582	4	US-09-702-705-334	Sequence 334, App
142	185.5	10.3	642	1	US-08-217-299-1	Sequence 1, Appli	215	163.5	9.1	582	4	US-09-736-457-334	Sequence 334, App
143	185.5	10.3	698	2	US-08-602-725-36	Sequence 36, Appl	216	163.5	9.1	582	4	US-09-614-124B-334	Sequence 334, App
144	185.5	10.3	702	4	US-09-949-016-6484	Sequence 6484, Ap	217	163.5	9.1	582	4	US-09-671-325-334	Sequence 334, App
145	185.5	10.3	734	2	US-08-389-459A-17	Sequence 17, Appl	218	163.5	9.1	582	4	US-09-589-184-334	Sequence 334, App
146	185.5	10.3	734	3	US-08-987-867A-17	Sequence 17, Appl	219	163.5	9.1	582	4	US-09-658-824-334	Sequence 334, App
147	185.5	10.3	740	4	US-09-949-016-8168	Sequence 8168, Ap	220	163.5	9.1	604	4	US-09-949-016-9548	Sequence 9548, Ap
148	185	10.2	1381	3	US-09-540-245A-16	Sequence 16, Appl	221	163.5	9.1	623	4	US-09-949-016-11206	Sequence 11206, A
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150	184.5	10.2	66	2	US-08-414-657D-55	Sequence 55, Appl	223	163.5	9.1	1745	4	US-09-800-729-89	Sequence 89, Appl
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152	184.5	10.2	404	4	US-09-638-648-3	Sequence 3, Appli	225	163	9.0	924	1	US-08-656-984A-28	Sequence 28, Appl
153	184	10.2	373	4	US-09-823-038A-60	Sequence 60, Appl	226	163	9.0	924	1	US-08-485-604-28	Sequence 28, Appl
154	184	10.2	405	4	US-08-755-235-4	Sequence 4, Appli	227	163	9.0	924	2	US-08-487-595-28	Sequence 28, Appl
155	182	10.1	626	4	US-09-949-016-6213	Sequence 6213, Ap	228	162	9.0	321	6	5169835-17	Patent No. 5169835
156	182	10.1	664	4	US-09-949-016-7850	Sequence 7850, Ap	229	162	9.0	321	6	5169835-17	Patent No. 5169835
157	179	9.9	300	4	US-09-254-465A-10	Sequence 10, Appl	230	161	8.9	622	4	US-09-499-846-2	Sequence 2, Appli
158	179	9.9	300	4	US-09-397-243D-12	Sequence 12, Appl	231	161	8.9	806	2	US-08-443-861-5	Sequence 5, Appli
159	179	9.9	300	4	US-09-953-499-10	Sequence 10, Appl	240	161	8.9	806	2	US-08-443-861-5	Sequence 5, Appli
160	174	9.6	261	4	US-09-270-767-32898	Sequence 32, Appl	241	161	8.9	806	3	US-08-193-829B-5	Sequence 5, Appli
161	174	9.6	261	4	US-09-270-767-48115	Sequence 48115, A	242	161	8.9	816	1	US-07-640-029-1	Sequence 1, Appli
162	171.5	9.5	780	1	US-08-232-538-14	Sequence 14, Appl	243	161	8.9	820	1	US-07-921-807B-3	Sequence 3, Appli
163	171.5	9.5	780	2	US-08-786-164-14	Sequence 14, Appl	244	161	8.9	820	3	US-08-441-944A-3	Sequence 3, Appli
164	171.5	9.5	1338	3	US-08-750-141A-3	Sequence 3, Appli	245	161	8.9	820	3	US-08-439-992A-1	Sequence 1, Appli
165	171.5	9.5	1338	4	US-09-119-014D-6	Sequence 6, Appli	246	161	8.9	1367	2	US-08-443-861-2	Sequence 2, Appli
166	171	9.5	464	2	US-08-602-725-32	Sequence 32, Appl	247	161	8.9	1367	3	US-08-193-829B-2	Sequence 2, Appli
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168	171	9.5	464	4	US-09-949-016-7525	Sequence 7525, Ap	249	160	8.9	270	4	US-09-254-465A-24	Sequence 24, Appl
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170	171	9.5	917	1	US-08-481-130-2	Sequence 2, Appli	251	160	8.9	273	4	US-09-254-465A-26	Sequence 26, Appl
171	171	9.5	917	1	US-08-656-984A-2	Sequence 2, Appli	252	160	8.9	273	4	US-09-953-499-26	Sequence 26, Appl
172	171	9.5	917	1	US-08-485-604-2	Sequence 2, Appli	253	160	8.9	319	1	US-08-597-495B-22	Sequence 22, Appl
173	171	9.5	917	1	US-08-485-604-2	Sequence 2, Appli	254	160	8.9	319	3	US-09-068-051A-22	Sequence 22, Appl
174	171	9.5	1253	3	US-08-506-296B-14	Sequence 14, Appl	256	160	8.9	319	4	US-09-336-536-67	Sequence 67, Appl
175	170	9.4	318	3	US-09-068-051A-32	Sequence 32, Appl	257	160	8.9	319	4	US-09-254-465A-6	Sequence 6, Appli
176	167.5	9.3	280	4	US-09-270-767-43068	Sequence 43068, A	257	160	8.9	319	4	US-09-953-499-6	Sequence 6, Appli
177	167.5	9.3	466	2	US-08-432-016-4	Sequence 4, Appli	258	160	8.9	609	4	US-09-949-016-7747	Sequence 7747, Ap
178	167.5	9.3	466	2	US-08-684-594-4	Sequence 4, Appli	259	160	8.9	609	4	US-09-949-016-7748	Sequence 7748, Ap
179	167	9.2	668	1	US-08-232-538-13	Sequence 13, Appl	260	160	8.9	609	4	US-09-949-016-7749	Sequence 7749, Ap
180	167	9.2	668	2	US-08-786-164-13	Sequence 13, Appl	261	160	8.9	609	4	US-09-949-016-7750	Sequence 7750, Ap
181	167	9.2	764	3	US-09-142-956B-14	Sequence 14, Appl	262	160	8.9	609	4	US-09-949-016-7751	Sequence 7751, Ap
182	167	9.2	767	2	US-08-874-678-2	Sequence 2, Appli	263	160	8.9	609	4	US-09-949-016-7752	Sequence 7752, Ap
183	167	9.2	767	3	US-08-643-839-2	Sequence 2, Appli	264	160	8.9	609	4	US-09-949-016-7753	Sequence 7753, Ap
184	167	9.2	767	3	US-08-848-886-2	Sequence 2, Appli	265	160	8.9	609	4	US-09-949-016-7754	Sequence 7754, Ap
185	167	9.2	788	1	US-08-232-538-15	Sequence 15, Appl	266	160	8.9	817	1	US-07-640-029-2	Sequence 2, Appli
186	167	9.2	788	2	US-08-786-164-15	Sequence 15, Appl	267	160	8.9	822	1	US-07-921-807B-4	Sequence 4, Appli
187	167	9.2	1356	1	US-08-810-116-8	Sequence 8, Appli	268	160	8.9	822	1	US-08-459-296-2	Sequence 2, Appli
188	167	9.2	1356	2	US-07-930-548A-8	Sequence 8, Appli	269	160	8.9	822	1	US-08-441-944A-4	Sequence 4, Appli
189	167	9.2	1356	3	US-09-098-707A-2	Sequence 2, Appli	270	160	8.9	822	2	US-08-451-822A-12	Sequence 12, Appl
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191	167	9.2	1356	4	US-09-949-016-6198	Sequence 6198, Ap	272	160	8.9	822	3	US-08-323-430-12	Sequence 12, Appl
192	167	9.2	1456	4	US-09-949-016-9953	Sequence 9953, Ap	273	159	8.8	822	1	US-07-997-133-1	Sequence 1, Appli
193	166.5	9.2	302	4	US-09-877-730-14	Sequence 14, Appl	274	158.5	8.8	1474	4	US-09-677-046A-4	Sequence 4, Appli
194	166.5	9.2	380	4	US-09-877-730-4	Sequence 4, Appli	275	158.5	8.8	1509	4	US-09-677-046A-2	Sequence 2, Appli
195	166	9.2	758	2	US-08-874-678-1	Sequence 1, Appli	276	158	8.7	292	4	US-09-800-729-175	Sequence 175, App
196	166	9.2	758	3	US-08-643-839-1	Sequence 1, Appli	277	158	8.7	611	2	US-08-752-307B-10	Sequence 10, Appl
197	166	9.2	758	3	US-09-051-363-24	Sequence 24, Appl	278	158	8.7	611	3	US-09-707-802-10	Sequence 10, Appl
198	166	9.2	758	3	US-09-348-886-1	Sequence 1, Appli	279	158	8.7	611	3	US-09-991-326-10	Sequence 10, Appl
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201	165.5	9.2	486	2	US-08-432-016-6	Sequence 6, Appli	282	157	8.7	260	4	US-09-254-465A-23	Sequence 23, Appl
202	165.5	9.2	486	2	US-08-684-594-6	Sequence 6, Appli	283	157	8.7	260	4	US-09-953-499-23	Sequence 23, Appl
							284	157	8.7	263	4	US-09-254-465A-25	Sequence 25, Appl

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(without alignments)
1116.490 Million cell updates/sec

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Searched: 513545 seqs, 74649064 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Issued first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	926.5	51.3	338	4	US-09-135-080-4
7	923.5	51.1	325	2	US-08-414-657D-2
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13	907	50.2	315	2	US-08-414-657D-47
14	905	50.1	310	2	US-08-414-657D-45
15	902	49.9	304	2	US-08-414-657D-48
16	886.5	49.1	287	2	US-08-414-657D-44
17	885.5	49.0	287	2	US-08-414-657D-49
18	796.5	44.1	252	2	US-08-414-657D-56
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21	276	15.3	588	4	US-09-949-016-10547
22	267	14.8	58	4	US-09-513-999C-6852
23	261	14.5	1395	3	US-09-540-245A-15
24	256	14.2	421	2	US-08-659-984A-1
25	256	14.2	421	3	US-08-660-531-1
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43	237	13.1	73	2	US-08-414-657D-51	Sequence 51, Appl
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51	225.5	12.5	860	5	PCT-US95-08493-19	Sequence 19, Appl
52	225.5	12.5	868	5	PCT-US95-08493-21	Sequence 21, Appl
53	225	12.5	4391	4	US-10-006-011A-2	Sequence 2, Appl
54	224.5	12.4	869	4	US-09-715-249-8	Sequence 8, Appl
55	222.5	12.3	504	4	US-09-270-767-43244	Sequence 43244, A
73	220.5	12.2	423	4	US-09-778-510-22	Sequence 22, Appl
76	220.5	12.2	440	4	US-09-944-457-61	Sequence 61, Appl
77	220.5	12.2	442	4	US-09-778-510-20	Sequence 20, Appl
78	220.5	12.2	442	4	US-09-930-803-1	Sequence 1, Appl
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91	212	11.7	59	2	US-08-414-657D-52	Sequence 52, Appl
92	212	11.7	59	2	US-08-414-657D-53	Sequence 53, Appl
93	211.5	11.7	1070	4	US-09-961-403-3	Sequence 3, Appl
94	211.5	11.7	1461	4	US-09-976-594-531	Sequence 531, App
95	211	11.7	398	4	US-09-778-510-4	Sequence 4, Appl
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111	197.5	10.9	1447	3	US-09-041-886-25	Sequence 25, Appl
112	197.5	10.9	1447	5	PCT-US94-05277-2	Sequence 2, Appl
113	197	10.9	1297	3	US-09-540-245A-17	Sequence 17, Appl
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122	192.5	10.7	826	4	US-09-877-730-16	Sequence 16, Appl
123	192.5	10.7	904	4	US-09-877-730-6	Sequence 6, Appl
124	192.5	10.7	907	4	US-09-877-730-20	Sequence 20, Appl
125	192.5	10.7	983	3	US-09-412-554A-2	Sequence 2, Appl
126	192.5	10.7	985	4	US-09-877-730-10	Sequence 10, Appl
127	192.5	10.7	991	4	US-09-877-730-12	Sequence 12, Appl
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PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1493
ID ABU10526 standard; protein; 440 AA.
DE Human secreted/transmembrane protein #17.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1494
ID ABU11312 standard; protein; 440 AA.
DE Human pro355 protein sequence.
PN US2002127643-A1.

PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1495
ID ABU67131 standard; protein; 440 AA.
DE Human PRO polypeptide #11.
PN US2002165143-A1.
PD 07-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1496
ID ABU95535 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1497
ID ABU96744 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1498
ID ABR70589 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1499
ID ABO04940 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1500
ID ABO08348 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US200304922-A1.
PD 06-MAR-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;

RESULT 1474
ID ABU98449 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PX US2003022301-A1.
PN 30-JAN-2003.
Query Match Similarity 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e+10;
RESULT 1475
ID ABR65848 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PX US2003036165-A1.
PN 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e+10;
RESULT 1476
ID ABR64565 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PX US2003027262-A1.
PN 20-FEB-2003.
PD 06-FEB-2003.
Query Match Similarity 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e+10;
RESULT 1477
ID ABUT9490 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PX US2003032110-A1.
PN 13-FEB-2003.
Query Match Similarity 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e+10;
RESULT 1478
ID AU952881 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PX US2003036142-A1.
PN 20-FEB-2003.
Query Match Similarity 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e+10;
RESULT 1479
ID ABUS95840 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PX US2003036145-A1.
PN 20-FEB-2003.
Query Match Similarity 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e+10;
RESULT 1480
ID ABUN91060 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PX US2003036154-A1.
PN 20-FEB-2003.
Query Match Similarity 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e+10;
RESULT 1481
ID ABUN90153 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PX US2003036153-A1.
PN 20-FEB-2003.
Query Match Similarity 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e+10;
RESULT 1482
ID ABON9568 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PX US2003044931-A1.
PN 06-MAR-2003.
Query Match Similarity 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e+10;
RESULT 1483
ID ABOL0840 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PX US2003036150-A1.
PN 20-FEB-2003.
Query Match Similarity 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e+10;
RESULT 1484
ID ABR70894 standard; protein; 440 AA.

DE Human secreted/transmembrane protein (PRO) #17.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1444
ID ABU94915 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1445
ID ABU90463 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1446
ID ABU83974 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1447
ID ABU93625 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1448
ID ABR64870 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1449
ID ABR68702 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1450
ID ABO06518 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1451
ID ABR99063 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1452
ID ABU56311 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, PRO355.
PN US2002132981-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1453
ID ABU56947 standard; protein; 440 AA.
DE Human PRO polypeptide #17.

PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1454
ID ABU85899 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1455
ID ABU82186 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1456
ID ABU87197 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1457
ID ABU83669 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1458
ID ABO08043 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1459
ID ABU60351 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2002168715-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1460
ID ABU81754 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1461
ID ABU65918 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1462
ID ABR59747 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1463
ID ABU93935 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036155-A1.
PD 20-FEB-2003.

RESULT 1423
ID ABO07433 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1424
ID ABO03620 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1425
ID ABR67068 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027286-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1426
ID ABO15671 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1427
ID ABUS5952 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, PRO355.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1428
ID ABUS6280 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1429
ID ABUS9225 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1430
ID ABU71128 standard; protein; 440 AA.
DE Human PRO355 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1431
ID ABO07738 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1432
ID ABR69979 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1433

ID ABR69312 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1434
ID ABO01453 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1435
ID ABUS1255 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1436
ID ABR60052 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1437
ID ABR67787 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1438
ID ABR65175 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1439
ID ABR68397 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1440
ID ABR71809 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1441
ID ABUS5289 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1442
ID ABUS8979 standard; protein; 440 AA.
DE - Human secreted/transmembrane protein (PRO) #17.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1443
ID ABUS3059 standard; protein; 440 AA.

Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1403
ID ABO18822 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1404
ID ABR78243 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1405
ID ABU64926 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO355.
PN US2002173463-A1.
PD 21-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1406
ID ABU84979 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1407
ID ABO00118 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1408
ID ABO11450 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1409
ID ABO02095 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1410
ID ABU58360 standard; protein; 440 AA.
DE Novel human secreted protein PRO355.
PN US2002150976-A1.
PD 17-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1411
ID ABU88669 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1412
ID ABU83364 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match

Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1413
ID ABO06165 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1414
ID ABR59201 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1415
ID ABO09263 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1416
ID ABO19127 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1417
ID ABO11145 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1418
ID ABR66763 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1419
ID ABO15976 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1420
ID ABO13682 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1421
ID ABU57246 standard; protein; 440 AA.
DE Human PRO355 protein.
PN US2002142958-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;
RESULT 1422
ID ABU65585 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, SEQ ID 34.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;

Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1383
ID ABR68092 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027284-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1384
ID ABU96145 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1385
ID ABU92576 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1386
ID ABO08653 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1387
ID ABO02705 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1388
ID ABR74859 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1389
ID ABR94621 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1390
ID ABU60240 standard; protein; 440 AA.
DE Human PRO polypeptide #11.
PN US2002132768-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1391
ID ABU85594 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1392
ID ABU98754 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;

Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1393
ID ABU97969 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1394
ID ABU91675 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1395
ID ABU89368 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1396
ID ABU86209 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1397
ID ABU67422 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1398
ID ABU80450 standard; protein; 440 AA.
DE Human PRO protein #17.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1399
ID ABR99368 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1400
ID ABR98758 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1401
ID ABO16281 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1402
ID ABR92181 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;

PD 20-MAR-2003.
PA (NIJ/) NI J.
PA (YOUNG/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSEN/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEI/) WEI Y.
PA (GREENE/) GREENE J M.
PA (RUBEN/) RUBEN S M.
PA (LIUD/) LIU D.
PA (CROCK/) CROCKER P R.
Query Match 12.2%; Score 220.5; DB 6; Length 364;
Best Local Similarity 26.0%; Pred. No. 2.7e-10;
RESULT 1366
ID ADE86598 standard; protein; 364 AA.
DE Novel human secreted protein #11.
PN US2003129895-A1.
PD 10-JUL-2003.
PA (NIJ/) NI J.
PA (YOUNG/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSEN/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEI/) WEI Y.
PA (GREENE/) GREENE J M.
PA (RUBEN/) RUBEN S M.
Query Match 12.2%; Score 220.5; DB 8; Length 364;
Best Local Similarity 26.0%; Pred. No. 2.7e-10;
RESULT 1367
ID ADR41469 standard; protein; 370 AA.
DE Human CD-like molecule HATCZ07, SEQ ID NO:268.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.2%; Score 220.5; DB 5; Length 370;
Best Local Similarity 26.0%; Pred. No. 2.7e-10;
RESULT 1368
ID AAM23691 standard; protein; 402 AA.
DE Human EST encoded protein SEQ ID NO: 1216.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSEQ-) HYSEQ INC.
Query Match 12.2%; Score 220.5; DB 4; Length 402;
Best Local Similarity 26.0%; Pred. No. 3.1e-10;
RESULT 1369
ID AA45093 standard; protein; 423 AA.
DE Mouse lymphoid derived dendritic cell adhesion molecule.
PN WO200008158-A2.
PD 17-FEB-2000.
PA (IMMUNEX) IMMUNEX CORP.
Query Match 12.2%; Score 220.5; DB 3; Length 423;
Best Local Similarity 26.0%; Pred. No. 3.3e-10;
RESULT 1370
ID ABO84564 standard; protein; 425 AA.
DE Human cancer-associated protein HP16-039.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 12.2%; Score 220.5; DB 8; Length 425;
Best Local Similarity 26.0%; Pred. No. 3.3e-10;
RESULT 1371
ID AAV17830 standard; protein; 440 AA.
DE Human PRO355 protein sequence.
PN WO9928462-A2.
PD 10-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 2; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1372
ID AAB01321 standard; protein; 440 AA.
DE Human PRO355 polypeptide.
PN WO200032776-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 3; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1373
ID AAU29040 standard; protein; 440 AA.
DE Human PRO polypeptide sequence #17.
PN WO20016848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 4; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1374
ID ABUS8416 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003027272-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1375
ID ABUS7964 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032127-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1376
ID ABUS4279 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003032112-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1377
ID ABR66153 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027278-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1378
ID ABR65543 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036159-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1379
ID ABUS9483 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003040070-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1380
ID ABUS5930 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO355.
PN US2002142959-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1381
ID ABUS2722 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032113-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1382
ID ABUS9843 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036147-A1.
PD 20-FEB-2003.

PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHYER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYN/) ROY M A.
PA (STEN/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1350
ID ADA55073 standard; protein; 1251 AA.
DE Human protein, SEQ ID 2641.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.4%; Score 224; DB 6; Length 1251;
Best Local Similarity 25.9%; Pred. No. 7.3e-10;
RESULT 1351
ID ABU1674 standard; protein; 380 AA.
DE Human MDDT polypeptide SEQ ID 621.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.3%; Score 223; DB 6; Length 380;
Best Local Similarity 26.4%; Pred. No. 1.7e-10;
RESULT 1352
ID AAY53028 standard; protein; 414 AA.
DE Human secreted protein clone cw1000_2 protein sequence SEQ ID NO:62.
PN WO9957132-A1.
PD 11-NOV-1999.
PA (GEMY) GENETICS INST INC.
Query Match 12.3%; Score 223; DB 3; Length 414;
Best Local Similarity 24.9%; Pred. No. 1.9e-10;
RESULT 1353
ID ABJ20228 standard; protein; 798 AA.
DE Human IG gene related protein SEQ ID NO 51.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 12.3%; Score 223; DB 6; Length 798;
Best Local Similarity 24.8%; Pred. No. 4.8e-10;
RESULT 1354
ID ABB97578 standard; protein; 1179 AA.
DE Novel human protein SEQ ID NO: 846.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 12.3%; Score 223; DB 5; Length 1179;
Best Local Similarity 24.8%; Pred. No. 8.2e-10;
RESULT 1355
ID ADR28014 standard; protein; 1179 AA.
DE Long form IGSF9 protein.
PN WO2004066933-A2.
PD 12-AUG-2004.
PA (MCLA/) MCLACHLAN K.
PA (GLAS/) GLASER S.
PA (PEAC/) PEACH R J.
PA (ROWE/) ROWE T.
Query Match 12.3%; Score 223; DB 8; Length 1179;
Best Local Similarity 24.8%; Pred. No. 8.2e-10;
RESULT 1356
ID ADR28013 standard; protein; 1179 AA.
DE Long form full-length IGSF9 protein.
PN WO2004066933-A2.
PD 12-AUG-2004.
PA (MCLA/) MCLACHLAN K.
PA (GLAS/) GLASER S.
PA (PEAC/) PEACH R J.

PA (ROWE/) ROWE T.
Query Match 12.3%; Score 223; DB 8; Length 1179;
Best Local Similarity 24.8%; Pred. No. 8.2e-10;
RESULT 1357
ID ADR09753 standard; protein; 595 AA.
DE Human protein useful for treating neurological disease Seq 3259.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.3%; Score 222; DB 8; Length 595;
Best Local Similarity 27.2%; Pred. No. 3.9e-10;
RESULT 1358
ID ABB10202 standard; protein; 744 AA.
DE Human cDNA SEQ ID NO: 510.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.3%; Score 222; DB 4; Length 744;
Best Local Similarity 23.6%; Pred. No. 5.3e-10;
RESULT 1359
ID ABP66789 standard; protein; 744 AA.
DE Human polypeptide SEQ ID NO 510.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 12.3%; Score 222; DB 5; Length 744;
Best Local Similarity 23.6%; Pred. No. 5.3e-10;
RESULT 1360
ID ADH72194 standard; protein; 1068 AA.
DE Human protein of the invention NOV51d SEQ ID NO:1090.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.3%; Score 222; DB 8; Length 1068;
Best Local Similarity 24.2%; Pred. No. 8.7e-10;
RESULT 1361
ID AAM42087 standard; protein; 1571 AA.
DE Human Down syndrome-cell adhesion molecule DS-CAM2.
PN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Query Match 12.2%; Score 221; DB 2; Length 1571;
Best Local Similarity 28.6%; Pred. No. 1.8e-09;
RESULT 1362
ID AAW42086 standard; protein; 1910 AA.
DE Human Down syndrome-cell adhesion molecule DS-CAM1.
PN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Query Match 12.2%; Score 221; DB 2; Length 1910;
Best Local Similarity 28.6%; Pred. No. 2.3e-09;
RESULT 1363
ID ADK71092 standard; protein; 2012 AA.
DE Human MP21 polypeptide.
PN WO2004015073-A2.
PD 19-FEB-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 12.2%; Score 221; DB 8; Length 2012;
Best Local Similarity 28.6%; Pred. No. 2.5e-09;
RESULT 1364
ID AAB25586 standard; protein; 364 AA.
DE Protein encoded by human secreted protein gene #11.
PN WO200029435-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.2%; Score 220.5; DB 3; Length 364;
Best Local Similarity 26.0%; Pred. No. 2.7e-10;
RESULT 1365
ID ADA27058 standard; protein; 364 AA.
DE Human novel secreted protein from cDNA HOUDJ81 #1.
PN US2003055231-A1.

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Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1336
ID ADJ63563 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1337
ID ADM30007 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1338
ID ADJ77458 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1339
ID ADJ65580 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1340
ID ADM27716 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1341
ID ADM42440 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1342
ID ADO06329 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1343
ID ADM28302 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1344
ID ADRI1181 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1345
ID ADRI8090 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1346
ID ADI95784 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1347
ID ADI96336 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1348
ID ADT03766 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1349
ID ADS74729 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein #56.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
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PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1320
ID ADH60006 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1321
ID ADH07034 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1322
ID ADH18141 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1323
ID ADH18776 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003152959-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1324
ID ADH13755 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1325
ID ADG09884 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1326
ID ADH97555 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1327
ID ADH15355 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207382-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1328
ID ADG09232 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1329
ID ADH65923 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1330
ID ADH14687 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1331
ID ADH60666 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1332
ID ADH18282 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1333
ID ADJ99723 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1334
ID ADL08916 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1335
ID ADM25257 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;

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PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1302
ID ADG81094 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1303
ID ADG57989 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1304
ID ADG53573 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1305
ID ADG71459 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1306
ID ADG81646 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1307
ID ADH30608 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US200307723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1308
ID ADH11975 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1309
ID ADG52397 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1310
ID ADG54125 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1311
ID ADG81094 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1312
ID ADG56333 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1313
ID ADH12599 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1314
ID ADG61445 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1315
ID ADH28532 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003202331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1316
ID ADG54677 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1317
ID ADG59717 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1318
ID ADH20606 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1319
ID ADH07461 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
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DE Novel human secreted and transmembrane protein PRO326.
PN US2003207424-A1.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1284
ID ADG15528 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003219885-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1285
ID ADF96926 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1286
ID ADG06111 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1287
ID ADG23695 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1288
ID ADG03984 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1289
ID ADG4885 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1290
ID ADG07182 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1291
ID ADG07734 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1292
ID ADG55229 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.

PN US2003194778-A1.
PA 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1293
ID ADG60893 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1294
ID ADG61997 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1295
ID ADG32390 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1296
ID ADG82198 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1297
ID ADG57437 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1298
ID ADG56885 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1299
ID ADG55781 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1300
ID ADG58541 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1301
ID ADG70907 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207420-A1.

Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1266
 ID ADE91689 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003199058-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1267
 ID ADE99107 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003211568-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1268
 ID ADG40577 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003225253-A1.
 PD 04-DEC-2003.
 PA (DESN/) DESNOYERS L.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOFSKI P J.
 PA (GURN/) GURNEY A L.
 PA (MATH/) MATHER J P.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1269
 ID ADF73971 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003180312-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1270
 ID ADG02268 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003207352-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1271
 ID ADG22054 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003207360-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1272
 ID ADG20124 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003207376-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1273
 ID ADF98030 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003207422-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1274

ID ADG24247 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003207426-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1275
 ID ADF98601 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003208055-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1276
 ID ADG03432 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003207351-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1277
 ID ADF99153 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003207353-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1278
 ID ADG16738 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003207359-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1279
 ID ADG05197 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003207375-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1280
 ID ADG19464 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003207425-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1281
 ID ADF73547 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003166051-A1.
 PD 04-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1282
 ID ADG13301 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003207357-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1283
 ID ADG08358 standard; protein; 1119 AA.

PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1248
ID ADE73472 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1249
ID ADE23329 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1250
ID ADE23881 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1251
ID ADE24524 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1252
ID ADD87349 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1253
ID ADE89215 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199082-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1254
ID ADE74007 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1255
ID ADE18354 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194784-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1256
ID ADE88663 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199054-A1.
PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1257
ID ADE99561 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1258
ID ADE94683 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1259
ID ADE91094 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1260
ID ADE95235 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1261
ID ADE93345 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1262
ID ADF34926 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1263
ID ADE98680 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1264
ID ADE92241 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1265
ID ADE90542 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;

DE Human secreted/transmembrane protein, #56.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1230
ID ADI64053 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1231
ID ADI65002 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1232
ID ADI63501 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1233
ID ADH81915 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1234
ID ADJ26457 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1235
ID ADJ26457 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1236
ID ADM82532 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1237
ID ADNI5931 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1238
ID ADNI6560 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.

PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1239
ID ADNI5379 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1240
ID ADNI4827 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1241
ID ADC81089 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1242
ID ADE79372 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1243
ID ADJ76537 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1244
ID ADD79901 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1245
ID ADD86305 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1246
ID ADE79796 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1247
ID ADE75753 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003211571-A1.

RESULT 1211
ID AD95891 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1212
ID ADE22777 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199084-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1213
ID ADD78895 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1214
ID ADE32845 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1215
ID ADE42537 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1216
ID ADD80553 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1217
ID AD99581 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1218
ID ADE40865 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1219
ID ADE04664 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1220

ID ADE92793 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1221
ID ADG21502 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1222
ID ADG23143 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1223
ID ADF97478 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1224
ID ADG80542 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1225
ID ADG79990 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1226
ID ADH59410 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1227
ID ADH55282 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1228
ID ADH55834 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1229
ID ADI38189 standard; protein; 1119 AA.

Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1193
ID AD54169 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
FN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1194
ID AD92486 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
FN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1195
ID AD91382 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
FN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1196
ID AD80396 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
FN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1197
ID AD32293 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
FN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1198
ID AD22225 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
FN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1199
ID AD79449 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
FN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1200
ID AD841985 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
FN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1201
ID AD17802 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
FN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;

Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1202
ID AD91934 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
FN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1203
ID AD33397 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
FN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1204
ID AD33949 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
FN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1205
ID AD80001 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
FN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1206
ID AD93038 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
FN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1207
ID AD19458 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
FN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1208
ID AD34927 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
FN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1209
ID AD18906 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
FN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1210
ID AD43102 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
FN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;

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PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1175
ID ADC48477 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1176
ID ADD10006 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1177
ID ADD04581 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087334-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1178
ID ADC80537 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1179
ID ADD11044 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1180
ID ADC47925 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1181
ID ADD05093 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1182
ID ADC79985 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1183
ID ADD09454 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1184
ID ADD04099 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1185
ID ADD03675 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1186
ID ADD41167 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1187
ID ADD52306 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1188
ID ADD53046 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1189
ID ADD53598 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1190
ID ADD51754 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1191
ID ADD02553 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1192
ID ADD01987 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
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DE Human secreted/transmembrane protein, #56.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1157
ID ADC13086 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1158
ID ADC50393 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1159
ID ADC71940 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1160
ID ADC59919 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1161
ID ADC52926 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1162
ID ADC57280 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1163
ID ADC60471 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1164
ID ADC50946 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1165
ID ADC65473 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.

PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1166
ID ADC54571 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1167
ID ADC53532 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1168
ID ADC59055 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1169
ID ADC55933 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1170
ID ADC58503 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1171
ID ADC12538 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1172
ID ADD03177 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1173
ID ADC90169 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1174
ID ADC69588 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194770-A1.

RESULT 1138
ID ADB47100 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1139
ID ADB66707 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1140
ID ADB77312 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1141
ID ADB34469 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1142
ID ADB35573 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1143
ID ADB33917 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1144
ID ADB35021 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1145
ID ADB36125 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1146
ID ADB46520 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1147

ID ADC28602 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1148
ID ADC39802 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1149
ID ADC40316 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1150
ID ADC19140 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1151
ID ADC34440 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1152
ID ADC29495 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1153
ID ADC29026 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1154
ID ADC40911 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1155
ID ADC19568 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1156
ID ADC34016 standard; protein; 1119 AA.

PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1120
ID ADA88587 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1121
ID ADA97592 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1122
ID ADB27349 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1123
ID ADB22282 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1124
ID ABO17606 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1125
ID ADA66973 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1126
ID ADB22834 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1127
ID ADB23607 standard; protein; 1119 AA.
DE Human PRO polypeptide SQ ID NO 352.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1128
ID ADA92329 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;

Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1129
ID ADB15392 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1130
ID ADB38644 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1131
ID ADB38092 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1132
ID ADB66564 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1133
ID ADB89644 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1134
ID ADB90376 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1135
ID ADB77820 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1136
ID ADB39477 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1137
ID ADB74956 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;

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DE Human PRO polypeptide SEQ ID NO 352.
PN US200307714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1102
ID ADA36488 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1103
ID ADA81060 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 7; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1104
ID ADA5936 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1105
ID ADB26245 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1106
ID ADB21730 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1107
ID ADA77509 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 7; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1108
ID ADB18249 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 7; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1109
ID ADA86932 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 7; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1110
ID ADA16754 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059909-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 7; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1111
ID ADA13183 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 7; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1112
ID ADA42051 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 7; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1113
ID ADA88035 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 7; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1114
ID ADA46423 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 7; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1115
ID ADA17398 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 7; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1116
ID ADA42901 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 7; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1117
ID ADB28453 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 7; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1118
ID ADB29005 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 7; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1119
ID ADA76957 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003059909-A1.
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RESULT 1083
ID ABO43324 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US200304945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1084
ID ADA74478 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1085
ID ADA42475 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1086
ID ADB24711 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1087
ID ADA82235 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1088
ID ADA75198 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1089
ID ADA85276 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1090
ID ADA84724 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1091
ID ABO17545 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1092
ID ADB24159 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1093
ID ADA80508 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1094
ID ADA75750 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1095
ID ADA46975 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1096
ID ADB25271 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1097
ID ADA93447 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1098
ID ADB26797 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1099
ID ADB31084 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1100
ID ADA61012 standard; protein; 1119 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1101
ID ADB24159 standard; protein; 1119 AA.
```


Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1065
ID ADA18355 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1066
ID ABO32807 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO326.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1067
ID ABO32808 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO332.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1068
ID ADA67525 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1069
ID ADB30532 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1070
ID ADA95828 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1071
ID ADA97040 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1072
ID ADA79344 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1073
ID ADA87483 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1074
ID ADB16685 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1075
ID ABO34867 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1076
ID ADA16330 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1077
ID ADA91777 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1078
ID ADB14840 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1079
ID ADB18801 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1080
ID ADA94016 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1081
ID ADB19912 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1082
ID ADB13224 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;

PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1047
ID ABU59826 standard; protein; 1119 AA.
DE Novel secreted and transmembrane protein PRO326.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1048
ID ABO25016 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein (PRO) #176.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1049
ID ABU64550 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #54.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1050
ID ABU67396 standard; protein; 1119 AA.
DE Human secreted protein PRO326.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1051
ID ABO14916 standard; protein; 1119 AA.
DE Human secreted / transmembrane polypeptide PRO326.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1052
ID ABU67021 standard; protein; 1119 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 352.
PN US2003021155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1053
ID ABU69673 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1054
ID ABO14855 standard; protein; 1119 AA.
DE Human secreted / transmembrane polypeptide PRO326.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1055
ID ADA45871 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003022328-A1.
PD 30-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1056
ID ADA76302 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1057
ID ADB29499 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1058
ID ADA18952 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1059
ID ADA61575 standard; protein; 1119 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1060
ID ADB19360 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1061
ID ADB27901 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1062
ID ADA86380 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1063
ID ADB15944 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1064
ID ADA47730 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1031
ID AAY08114 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 2; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1032
ID AAY70674 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO20015797-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 3; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1033
ID ADC78606 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 3; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1034
ID AAB80263 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1035
ID AAB48162 standard; protein; 1119 AA.
DE Human PRO326 polypeptide.
PN WO200075316-A1.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1036
ID AAU00827 standard; protein; 1119 AA.
DE Human immune response protein PRO326 (UNQ287).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1037
ID AAU12347 standard; protein; 1119 AA.
DE Human PRO326 polypeptide sequence.

PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1038
ID ABU71641 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1039
ID ABO17791 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1040
ID ABU71496 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1041
ID ABU81045 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1042
ID ABU71942 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO326.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1043
ID ABO01825 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1044
ID ABU66745 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US20030316180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1045
ID ABU54398 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO326.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1046
ID ABO47413 standard; protein; 1119 AA.
DE Human secreted/transmembrane polypeptide PRO326.
PN US2003044839-A1.

PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1017
ID ADI65492 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1018
ID ADI37751 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1019
ID ADH97551 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1020
ID ADI65919 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1021
ID ADH60662 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1022
ID ADJ99719 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1023
ID ADL08912 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1024
ID ADM25253 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1025
ID ADM30003 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1026
ID AD006325 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1027
ID ADR11177 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1028
ID ADR18086 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N P.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1029
ID ADT03762 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1030
ID ADS74725 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein #54.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.

Best Local Similarity				23.9%;	Pred. No. 5.8e-10;
RESULT 1009					
ID	ADF73543	standard; protein; 1059 AA.			
DE	Human secreted/transmembrane protein, #54.				
PN	US2003166051-A1.				
PD	04-SEP-2003.				
PA	(GETH) GENENTECH INC.				
Query Match			12.4%;	Score 224;	DB 8;
Best Local Similarity			23.9%;	Pred. No. 5.8e-10;	Length 1059;
RESULT 1010					
ID	ADG92386	standard; protein; 1059 AA.			
DE	Human secreted/transmembrane protein, #54.				
PN	US2003027145-A1.				
PD	06-FEB-2003.				
PA	(GETH) GENENTECH INC.				
Query Match			12.4%;	Score 224;	DB 8;
Best Local Similarity			23.9%;	Pred. No. 5.8e-10;	Length 1059;
RESULT 1011					
ID	ADG92413	standard; protein; 1059 AA.			
DE	Human secreted/transmembrane protein, #54.				
PN	US2003027146-A1.				
PD	06-FEB-2003.				
PA	(GETH) GENENTECH INC.				
Query Match			12.4%;	Score 224;	DB 8;
Best Local Similarity			23.9%;	Pred. No. 5.8e-10;	Length 1059;
RESULT 1012					
ID	ADH26602	standard; protein; 1059 AA.			
DE	Human secreted/transmembrane protein, #54.				
PN	US2004005553-A1.				
PD	08-JAN-2004.				
PA	(GETH) GENENTECH INC.				
Query Match			12.4%;	Score 224;	DB 8;
Best Local Similarity			23.9%;	Pred. No. 5.8e-10;	Length 1059;
RESULT 1013					
ID	ADH07457	standard; protein; 1059 AA.			
DE	Human secreted/transmembrane protein, #54.				
PN	US2004006211-A1.				
PD	08-JAN-2004.				
PA	(GETH) GENENTECH INC.				
Query Match			12.4%;	Score 224;	DB 8;
Best Local Similarity			23.9%;	Pred. No. 5.8e-10;	Length 1059;
RESULT 1014					
ID	ADH60002	standard; protein; 1059 AA.			
DE	Human secreted/transmembrane protein, #54.				
PN	US2003215904-A1.				
PD	20-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match			12.4%;	Score 224;	DB 8;
Best Local Similarity			23.9%;	Pred. No. 5.8e-10;	Length 1059;
RESULT 1015					
ID	ADH07030	standard; protein; 1059 AA.			
DE	Human secreted/transmembrane protein, #54.				
PN	US2004005665-A1.				
PD	08-JAN-2004.				
PA	(DESN) DESNOYERS L.				
PA	(GODD) GODDARD A.				
PA	(GODO) GODOWSKI P J.				
PA	(GURN) GURNEY A L.				
PA	(MATH) MATHER J P.				
PA	(WILL) WILLIAMS P M.				
PA	(WOOD) WOOD W I.				
Query Match			12.4%;	Score 224;	DB 8;
Best Local Similarity			23.9%;	Pred. No. 5.8e-10;	Length 1059;
RESULT 1016					
ID	AD118772	standard; protein; 1059 AA.			
DE	Human secreted/transmembrane protein, #54.				
PN	US2003152999-A1.				

DE Human secreted/transmembrane protein, #54.
PN US2003059828-A1.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 983
ID ADC40312 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 984
ID ADC19136 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 985
ID ADC34436 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 986
ID ADC29491 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 987
ID ADC29022 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 988
ID ADC40907 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 989
ID ADC19564 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 990
ID ADC34012 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 991
ID ADC13082 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.

PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 992
ID ADC12534 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 993
ID AD005089 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 994
ID AD004095 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 995
ID AD003671 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 996
ID AD834923 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 997
ID ADH59406 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 998
ID ADI38185 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 999
ID ADJ26453 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1000
ID ADE79368 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003135025-A1.

RESULT 964
ID ABOU69671 standard; protein; 1059 AA.
DE Novel human secreted and transmembrane protein PRO335.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 965
ID ABO14853 standard; protein; 1059 AA.
DE Human secreted / transmembrane polypeptide PRO335.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 966
ID ADB29495 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 967
ID ADA18351 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 968
ID ABO32805 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein PRO335.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 969
ID ABO34865 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 970
ID ADA16326 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 971
ID ADA42471 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 972
ID ABO17543 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 973
ID ADC39798 standard; protein; 1059 AA.

ID ADA16750 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 974
ID ADA13179 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 975
ID ADA42047 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 976
ID ADA17394 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 977
ID ADA42897 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 978
ID ABO17604 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 979
ID ADB77816 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 980
ID ADB74952 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 981
ID ADC28598 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 982
ID ADC39798 standard; protein; 1059 AA.

Query Match 12.4%; Score 224; DB 4; Length 434;
Best Local Similarity 25.5%; Pred. No. 1.7e-10;
RESULT 946
ID AAM93829 standard; protein; 697 AA.
DE Human polypeptide, SEQ ID NO: 3893.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.4%; Score 224; DB 4; Length 697;
Best Local Similarity 23.9%; Pred. No. 3.3e-10;
RESULT 947
ID ADJ31860 standard; protein; 697 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3893.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.4%; Score 224; DB 8; Length 697;
Best Local Similarity 23.9%; Pred. No. 3.3e-10;
RESULT 948
ID ABG02019 standard; protein; 737 AA.
DE Novel human diagnostic protein #2010.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 224; DB 4; Length 737;
Best Local Similarity 25.5%; Pred. No. 3.5e-10;
RESULT 949
ID AAY08095 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 2; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 950
ID AAY13393 standard; protein; 1059 AA.
DE Amino acid sequence of protein PRO335.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 2; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 951
ID AAY70672 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 3; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 952
ID ADC78602 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 3; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 953
ID AAB80261 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO2000104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 954
ID AAU00825 standard; protein; 1059 AA.
DE Human immune response protein PRO335 (UNQ287).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1059;

Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 955
ID ABU71639 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 956
ID ABU71494 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 957
ID ABU71940 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein PRO335.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 958
ID ABO01823 standard; protein; 1059 AA.
DE Novel human secreted and transmembrane protein PRO335.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 959
ID ABU54396 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein PRO335.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 960
ID ABO47411 standard; protein; 1059 AA.
DE Human secreted/transmembrane polypeptide PRO335.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 961
ID ABU64548 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #52.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 962
ID ABU67394 standard; protein; 1059 AA.
DE Human secreted protein PRO335.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 963
ID ABO14914 standard; protein; 1059 AA.
DE Human secreted / transmembrane polypeptide PRO335.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;

PA (AGEN-) AGENSYS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1171;
Best Local Similarity 25.3%; Pred. No. 6e-10;
RESULT 928
ID ADL16624 standard; protein; 1171 AA.
DE Human 282PiG3 polypeptide #56.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1171;
Best Local Similarity 25.3%; Pred. No. 6e-10;
RESULT 929
ID ADL16580 standard; protein; 1171 AA.
DE Human 282PiG3 polypeptide #33.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1171;
Best Local Similarity 25.3%; Pred. No. 6e-10;
RESULT 930
ID ADL16429 standard; protein; 1171 AA.
DE Human 282PiG3 polypeptide #2.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1171;
Best Local Similarity 25.3%; Pred. No. 6e-10;
RESULT 931
ID ADL16445 standard; protein; 1171 AA.
DE Human 282PiG3 polypeptide #11.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1171;
Best Local Similarity 25.3%; Pred. No. 6e-10;
RESULT 932
ID ADE35236 standard; protein; 1224 AA.
DE Human Protein AAB60937, SEQ ID NO 1049.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 12.4%; Score 224.5; DB 7; Length 1224;
Best Local Similarity 25.3%; Pred. No. 6.4e-10;
RESULT 933
ID ADL15032 standard; protein; 1224 AA.
DE Human neural cell adhesion molecule protein for cancer treatment.
PN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOT-) BIOINVENT INT AB.
Query Match 12.4%; Score 224.5; DB 7; Length 1224;
Best Local Similarity 25.3%; Pred. No. 6.4e-10;
RESULT 934
ID ADJ75519 standard; protein; 1224 AA.
DE Marker gene related amino acid sequence SEQ ID NO:771.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1224;
Best Local Similarity 25.3%; Pred. No. 6.4e-10;
RESULT 935
ID ADL16454 standard; protein; 1224 AA.
DE Human 282PiG3 polypeptide #20.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1224;
Best Local Similarity 25.3%; Pred. No. 6.4e-10;
RESULT 936
ID ADN04062 standard; protein; 1224 AA.
DE Antipsoriatic protein sequence #226.
PN WO2004028479-A2.
PD 08-APR-2004.

PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1224;
Best Local Similarity 25.3%; Pred. No. 6.4e-10;
RESULT 937
ID ADQ19766 standard; protein; 1224 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2585.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1224;
Best Local Similarity 25.3%; Pred. No. 6.4e-10;
RESULT 938
ID ADRI4776 standard; protein; 1224 AA.
DE Amino acid sequence of human MAPCAX orthologue #8.
PN WO2004066948-A2.
PD 12-AUG-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1224;
Best Local Similarity 25.3%; Pred. No. 6.4e-10;
RESULT 939
ID ADP29420 standard; protein; 1583 AA.
DE Human secreted protein SEQ ID #187.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1583;
Best Local Similarity 23.9%; Pred. No. 9.1e-10;
RESULT 940
ID ADP29354 standard; protein; 1583 AA.
DE Human secreted protein SEQ ID #121.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1583;
Best Local Similarity 23.9%; Pred. No. 9.1e-10;
RESULT 941
ID ABG20008 standard; protein; 1645 AA.
DE Novel human diagnostic protein #19999.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 224.5; DB 4; Length 1645;
Best Local Similarity 23.9%; Pred. No. 9.5e-10;
RESULT 942
ID ABG22631 standard; protein; 1765 AA.
DE Novel human diagnostic protein #22622.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 224.5; DB 4; Length 1765;
Best Local Similarity 23.9%; Pred. No. 1.1e-09;
RESULT 943
ID ABG12017 standard; protein; 1944 AA.
DE Novel human diagnostic protein #12008.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 224.5; DB 4; Length 1944;
Best Local Similarity 23.9%; Pred. No. 1.2e-09;
RESULT 944
ID AAE30259 standard; peptide; 68 AA.
DE Human LP289 protein immunoglobulin-like domain #1.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 12.4%; Score 224; DB 6; Length 68;
Best Local Similarity 65.7%; Pred. No. 1.4e-11;
RESULT 945
ID ABG02117 standard; protein; 434 AA.
DE Novel human diagnostic protein #2108.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 12.6%; Score 228; DB 4; Length 1483;
Best Local Similarity 24.1%; Pred. No. 4.1e-10;
RESULT 911
ID ADN22360 standard; protein; 6642 AA.
DE Bacterial polypeptide #5013.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.5%; Score 226; DB 8; Length 6642;
Best Local Similarity 23.7%; Pred. No. 4.8e-09;
RESULT 912
ID AAR32718 standard; protein; 478 AA.
DE Mouse muscle-localized protein-tyrosine-kinase receptor 5' fragment.
PN WO9602644-A1.
PD 01-FEB-1996.
PA (GENY) GENETICS INST INC.
Query Match 12.5%; Score 225.5; DB 2; Length 478;
Best Local Similarity 24.8%; Pred. No. 1.4e-10;
RESULT 913
ID AAR32716 standard; protein; 860 AA.
DE Mouse muscle-localised protein-tyrosine-kinase receptor-1 isoform.
PN WO9602644-A1.
PD 01-FEB-1996.
PA (GENY) GENETICS INST INC.
Query Match 12.5%; Score 225.5; DB 2; Length 860;
Best Local Similarity 24.8%; Pred. No. 3.2e-10;
RESULT 914
ID AAR32717 standard; protein; 868 AA.
DE Mouse muscle-localised protein-tyrosine-kinase receptor-2 isoform.
PN WO9602644-A1.
PD 01-FEB-1996.
PA (GENY) GENETICS INST INC.
Query Match 12.5%; Score 225.5; DB 2; Length 868;
Best Local Similarity 24.8%; Pred. No. 3.3e-10;
RESULT 915
ID ABJ10922 standard; protein; 869 AA.
DE Human secreted protein (SECP) #18.
PN WO200270669-A2.
PD 12-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.5%; Score 225.5; DB 5; Length 869;
Best Local Similarity 29.5%; Pred. No. 3.3e-10;
RESULT 916
ID AAE34390 standard; protein; 4391 AA.
DE Human perlecan protein.
PN WO200295415-A2.
PD 28-NOV-2002.
PA (OSTE-) OSTEOMETER BIO TECH AS.
Query Match 12.5%; Score 225; DB 6; Length 4391;
Best Local Similarity 25.7%; Pred. No. 3.3e-09;
RESULT 917
ID ABG74129 standard; protein; 537 AA.
DE Human hMusk-R deletion mutant mMusk-RI.
PN US2002150876-A1.
PD 17-OCT-2002.
PA (PIPP/) PIPPIG S D.
PA (VERE/) VERES G.
Query Match 12.4%; Score 224.5; DB 4; Length 537;
Best Local Similarity 26.0%; Pred. No. 2.1e-10;
RESULT 918
ID AAG77857 standard; protein; 537 AA.
DE Mutant protein mMusk-RI.
PN WO200172834-A1.
PD 04-OCT-2001.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 12.4%; Score 224.5; DB 4; Length 537;
Best Local Similarity 26.0%; Pred. No. 2.1e-10;
RESULT 919

ID ABG74130 standard; protein; 576 AA.
DE Human hMusk-R deletion mutant mMusk-RII.
PN US2002150876-A1.
PD 17-OCT-2002.
PA (PIPP/) PIPPIG S D.
PA (VERE/) VERES G.
Query Match 12.4%; Score 224.5; DB 4; Length 576;
Best Local Similarity 26.0%; Pred. No. 2.3e-10;
RESULT 920
ID AAG77858 standard; protein; 576 AA.
DE Mutant protein mMusk-RII.
PN WO200172834-A1.
PD 04-OCT-2001.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 12.4%; Score 224.5; DB 4; Length 576;
Best Local Similarity 26.0%; Pred. No. 2.3e-10;
RESULT 921
ID ABG74128 standard; protein; 869 AA.
DE Human muscle specific tyrosine kinase receptor, hMusk-R.
PN US2002150876-A1.
PD 25-MAY-2001.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 12.4%; Score 224.5; DB 4; Length 869;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 922
ID AAB68421 standard; protein; 869 AA.
DE Amino acid sequence of a human Musk-R polypeptide.
PN WO200136659-A2.
PD 25-MAY-2001.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 12.4%; Score 224.5; DB 4; Length 869;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 923
ID AAG77856 standard; protein; 869 AA.
DE Protein of muscle specific tyrosine kinase receptor (hMusk-R).
PN WO200172834-A1.
PD 04-OCT-2001.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 12.4%; Score 224.5; DB 4; Length 869;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 924
ID ADS17276 standard; protein; 869 AA.
DE Human muscle specific tyrosine kinase receptor (Musk-R) protein fragment.
PN US6790614-B1.
PD 14-SEP-2004.
PA (NOVS) NOVARTIS AG.
Query Match 12.4%; Score 224.5; DB 8; Length 869;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 925
ID ABG22633 standard; protein; 981 AA.
DE Novel human diagnostic protein #22624.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 224.5; DB 4; Length 981;
Best Local Similarity 23.9%; Pred. No. 4.7e-10;
RESULT 926
ID ADR08740 standard; protein; 1113 AA.
DE Human protein useful for treating neurological disease Seq 2246.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.4%; Score 224.5; DB 8; Length 1113;
Best Local Similarity 25.3%; Pred. No. 5.6e-10;
RESULT 927
ID ADI6578 standard; protein; 1171 AA.
DE Human 282P1G3 polypeptide #31.
PN WO2004016734-A2.
PD 26-FEB-2004.

PA (AGEN-) AGENSYS INC. 12.7%; Score 229.5; DB 8; Length 1224;
Query Match Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 893
ID ADL16591 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #38.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 894
ID ADL16620 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #52.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 895
ID ADL16456 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #22.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 896
ID ADL16615 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #50.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 897
ID ADL16622 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #54.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 898
ID ADL16444 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #10.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 899
ID ADL16458 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #24.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 900
ID ADL16550 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #27.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 901
ID ADL16459 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #25.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.

Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 902
ID ADL16603 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #44.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 903
ID ADL16453 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #19.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 904
ID ADL16632 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #63.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 905
ID ADL16609 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #47.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 906
ID ADQ39441 standard; protein; 3588 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1104.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.7%; Score 229; DB 8; Length 3588;
Best Local Similarity 26.0%; Pred. No. 1.1e-09;
RESULT 907
ID ADQ39440 standard; protein; 4346 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1103.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.7%; Score 229; DB 8; Length 4346;
Best Local Similarity 26.0%; Pred. No. 1.5e-09;
RESULT 908
ID ADQ39439 standard; protein; 4347 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1102.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.7%; Score 229; DB 8; Length 4347;
Best Local Similarity 26.0%; Pred. No. 1.5e-09;
RESULT 909
ID ADJ69461 standard; protein; 4370 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1267.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 12.7%; Score 229; DB 7; Length 4370;
Best Local Similarity 26.0%; Pred. No. 1.5e-09;
RESULT 910
ID ABG16336 standard; protein; 1483 AA.
DE Novel human diagnostic protein #16327.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 12.7%; Score 229.5; DB 8; Length 1183;
Query Match Similarity 25.6%; Pred. No. 2.3e-10;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 875
ID ADL16449 standard; protein; 1183 AA.
DE Human 282PiG3 polypeptide #15.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 876
ID ADL16602 standard; protein; 1183 AA.
DE Human 282PiG3 polypeptide #43.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 877
ID ADL16437 standard; protein; 1183 AA.
DE Human 282PiG3 polypeptide #6.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 878
ID ADL16448 standard; protein; 1208 AA.
DE Human 282PiG3 polypeptide #14.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 879
ID ADL16596 standard; protein; 1208 AA.
DE Human 282PiG3 polypeptide #40.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 880
ID ADL16435 standard; protein; 1208 AA.
DE Human 282PiG3 polypeptide #5.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 881
ID ADL16627 standard; protein; 1208 AA.
DE Human 282PiG3 polypeptide #59.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 882
ID ADL16598 standard; protein; 1208 AA.
DE Human 282PiG3 polypeptide #42.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 883
ID ADJ69602 standard; protein; 1224 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1408.
PN WO2003087768-A2.
PD 23-OCT-2003.

PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES. 12.7%; Score 229.5; DB 7; Length 1224;
Query Match Similarity 25.6%; Pred. No. 2.4e-10;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 884
ID ADL16443 standard; protein; 1224 AA.
DE Human 282PiG3 polypeptide #9.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 885
ID ADL16597 standard; protein; 1224 AA.
DE Human 282PiG3 polypeptide #41.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 886
ID ADL16621 standard; protein; 1224 AA.
DE Human 282PiG3 polypeptide #53.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 887
ID ADL16452 standard; protein; 1224 AA.
DE Human 282PiG3 polypeptide #18.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 888
ID ADL16623 standard; protein; 1224 AA.
DE Human 282PiG3 polypeptide #55.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 889
ID ADL16579 standard; protein; 1224 AA.
DE Human 282PiG3 polypeptide #32.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 890
ID ADL16427 standard; protein; 1224 AA.
DE Human 282PiG3 polypeptide #1.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 891
ID ADL16455 standard; protein; 1224 AA.
DE Human 282PiG3 polypeptide #21.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 892
ID ADL16457 standard; protein; 1224 AA.
DE Human 282PiG3 polypeptide #23.
PN WO2004016734-A2.
PD 26-FEB-2004.

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1105.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.7%; Score 230; DB 8; Length 4393;
Best Local Similarity 26.0%; Pred. No. 1.2e-09;
RESULT 857
ID ABG23265 standard; protein; 4436 AA.
DE Novel human diagnostic protein #23256.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.7%; Score 230; DB 4; Length 4436;
Best Local Similarity 26.0%; Pred. No. 1.2e-09;
RESULT 858
ID ADL16585 standard; protein; 849 AA.
DE Human 282PIG3 polypeptide #35.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 849;
Best Local Similarity 25.6%; Pred. No. 1.4e-10;
RESULT 859
ID ADL16586 standard; protein; 851 AA.
DE Human 282PIG3 polypeptide #36.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 851;
Best Local Similarity 25.6%; Pred. No. 1.4e-10;
RESULT 860
ID AAW26506 standard; protein; 869 AA.
DE Human Dmk receptor.
PN US5656473-A.
PD 12-AUG-1997.
PA (REG-) REGENERON PHARM INC.
Query Match 12.7%; Score 229.5; DB 2; Length 869;
Best Local Similarity 26.4%; Pred. No. 1.5e-10;
RESULT 861
ID AAW26611 standard; protein; 869 AA.
DE Human muscle-specific kinase (MUSK).
PN WO9721811-A2.
PD 19-JUN-1997.
PA (REG-) REGENERON PHARM INC.
Query Match 12.7%; Score 229.5; DB 2; Length 869;
Best Local Similarity 26.4%; Pred. No. 1.5e-10;
RESULT 862
ID ADQ89844 standard; protein; 869 AA.
DE Antagonist of cell cycle progression polypeptide #137.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 12.7%; Score 229.5; DB 8; Length 869;
Best Local Similarity 26.4%; Pred. No. 1.5e-10;
RESULT 863
ID ADL16446 standard; protein; 893 AA.
DE Human 282PIG3 polypeptide #12.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.5e-10;
RESULT 864
ID ADL16584 standard; protein; 893 AA.
DE Human 282PIG3 polypeptide #34.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.5e-10;
RESULT 865
ID ADL16625 standard; protein; 893 AA.
DE Human 282PIG3 polypeptide #57.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.5e-10;
RESULT 866
ID ADL16431 standard; protein; 893 AA.
DE Human 282PIG3 polypeptide #3.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.5e-10;
RESULT 867
ID ADL16626 standard; protein; 1117 AA.
DE Human 282PIG3 polypeptide #58.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.1e-10;
RESULT 868
ID ADL16590 standard; protein; 1117 AA.
DE Human 282PIG3 polypeptide #37.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.1e-10;
RESULT 869
ID ADL16447 standard; protein; 1117 AA.
DE Human 282PIG3 polypeptide #13.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.1e-10;
RESULT 870
ID ADL16433 standard; protein; 1117 AA.
DE Human 282PIG3 polypeptide #4.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.1e-10;
RESULT 871
ID ADL16592 standard; protein; 1117 AA.
DE Human 282PIG3 polypeptide #39.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.1e-10;
RESULT 872
ID ABM83685 standard; protein; 1171 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3934.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.7%; Score 229.5; DB 8; Length 1171;
Best Local Similarity 25.6%; Pred. No. 2.2e-10;
RESULT 873
ID ADL16604 standard; protein; 1183 AA.
DE Human 282PIG3 polypeptide #45.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 874
ID ADL16628 standard; protein; 1183 AA.
DE Human 282PIG3 polypeptide #60.
PN WO2004016734-A2.

RESULT 843
ID ADP67247 standard; protein; 1028 AA.
DE Human NB-3 protein.
PN WO2004052389-A2.
PD 24-JUN-2004.
PA (SAGE-) SINGAPORE GEN HOSPITAL PTE LTD.
PA (FORR/) FORREST G R.
Query Match 12.8%; Score 231; DB 8; Length 1028;
Best Local Similarity 26.7%; Pred. No. 1.4e-10;
RESULT 844
ID ADG39786 standard; protein; 3931 AA.
DE Human novel protein NOV9.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 12.8%; Score 231; DB 7; Length 3931;
Best Local Similarity 28.3%; Pred. No. 8.6e-10;
RESULT 845
ID AAW26507 standard; protein; 868 AA.
DE Rat Dmk receptor.
PN US5656473-A.
PD 12-AUG-1997.
PA (REGE-) REGENERON PHARM INC.
Query Match 12.8%; Score 230.5; DB 2; Length 868;
Best Local Similarity 25.2%; Pred. No. 1.2e-10;
RESULT 846
ID AAW26610 standard; protein; 868 AA.
DE Rat muscle-specific kinase (MUSK).
PN WO9721811-A2.
PD 19-JUN-1997.
PA (REGE-) REGENERON PHARM INC.
Query Match 12.8%; Score 230.5; DB 2; Length 868;
Best Local Similarity 25.2%; Pred. No. 1.2e-10;
RESULT 847
ID ADH71830 standard; protein; 961 AA.
DE Human protein of the invention NOV29ae SEQ ID NO:726.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 230.5; DB 8; Length 961;
Best Local Similarity 27.2%; Pred. No. 1.4e-10;
RESULT 848
ID ADH71832 standard; protein; 961 AA.
DE Human protein of the invention NOV29af SEQ ID NO:728.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 230.5; DB 8; Length 961;
Best Local Similarity 27.2%; Pred. No. 1.4e-10;
RESULT 849
ID ABO84727 standard; protein; 1040 AA.
DE Mouse cancer-associated protein MP22-025.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 12.8%; Score 230.5; DB 8; Length 1040;
Best Local Similarity 25.0%; Pred. No. 1.5e-10;
RESULT 850
ID ABO84469 standard; protein; 3475 AA.
DE Human cancer-associated protein HP13-036.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 12.8%; Score 230.5; DB 8; Length 3475;
Best Local Similarity 24.3%; Pred. No. 8.1e-10;
RESULT 851
ID ADG39842 standard; protein; 1928 AA.
DE Protein similar to human NOV9 #3.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 12.7%; Score 230; DB 7; Length 1928;
Best Local Similarity 22.9%; Pred. No. 4e-10;
RESULT 852
ID ADG39843 standard; protein; 1951 AA.
DE Protein similar to human NOV9 #4.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 12.7%; Score 230; DB 7; Length 1951;
Best Local Similarity 22.9%; Pred. No. 4e-10;
RESULT 853
ID AAY53667 standard; protein; 3117 AA.
DE Sequence gi/3328186 from an alignment with protein 608.
PN WO9960164-A1.
PD 25-NOV-1999.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 12.7%; Score 230; DB 3; Length 3117;
Best Local Similarity 22.9%; Pred. No. 7.7e-10;
RESULT 854
ID AAB31889 standard; protein; 4393 AA.
DE Amino acid sequence of a human protein.
PN WO200105422-A2.
PD 25-JAN-2001.
PA (INMR) BIOMERIEUX STELHYS.
Query Match 12.7%; Score 230; DB 4; Length 4393;
Best Local Similarity 26.0%; Pred. No. 1.2e-09;
RESULT 855
ID ADL35758 standard; protein; 4393 AA.
DE Human perlecan (heparan sulphate proteoglycan 2; HSPG2) protein.
PN WO2004019893-A2.
PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match 12.7%; Score 230; DB 8; Length 4393;
Best Local Similarity 26.0%; Pred. No. 1.2e-09;
RESULT 856
ID ADQ39442 standard; protein; 4393 AA.

RESULT 828
ID ADH71820 standard; protein; 2602 AA.
DE Human protein of the invention NOV29z SEQ ID NO:716.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2602;
Best Local Similarity 26.9%; Pred. No. 4e-10;
RESULT 829
ID ADJ83055 standard; protein; 2617 AA.
DE Human NOVX NOV12a protein.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBOOK J P.
PA (TCH/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 12.8%; Score 232; DB 7; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 830
ID ADH71842 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ak SEQ ID NO:738.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 831
ID ADH71852 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ap SEQ ID NO:748.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 832
ID ADH71838 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ai SEQ ID NO:734.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 833
ID ADH71770 standard; protein; 2617 AA.
DE Human protein of the invention NOV29a SEQ ID NO:666.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;

RESULT 834
ID ADH71836 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ah SEQ ID NO:732.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 835
ID ADH71840 standard; protein; 2617 AA.
DE Human protein of the invention NOV29aj SEQ ID NO:736.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 836
ID ADH71844 standard; protein; 2617 AA.
DE Human protein of the invention NOV29al SEQ ID NO:740.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 837
ID ADH71846 standard; protein; 2617 AA.
DE Human protein of the invention NOV29am SEQ ID NO:742.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 838
ID ADH71850 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ao SEQ ID NO:746.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 839
ID ADH71854 standard; protein; 2617 AA.
DE Human protein of the invention NOV29aq SEQ ID NO:750.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 840
ID ADH71848 standard; protein; 2617 AA.
DE Human protein of the invention NOV29an SEQ ID NO:744.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 841
ID ABU07377 standard; protein; 3931 AA.
DE Human protein NOV9.
PN WO200285922-A2.
PD 31-OCT-2002.
PA (CURA-) CURAGEN CORP.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 232; DB 6; Length 3931;
Best Local Similarity 28.3%; Pred. No. 7.1e-10;
RESULT 842
ID AAW29667 standard; protein; 1028 AA.
DE Homo sapiens DL185_1 clone secreted protein.
PN WO9830695-A2.
PD 16-JUL-1998.
PA (GENY-) GENETICS INST INC.
Query Match 12.8%; Score 231; DB 2; Length 1028;
Best Local Similarity 26.7%; Pred. No. 1.4e-10;

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.0%; Score 235.5; DB 8; Length 632;
Best Local Similarity 26.9%; Pred. No. 2.9e-11;
RESULT 815
ID ADH71818 standard; protein; 967 AA.
DE Human protein of the invention NOV29y SEQ ID NO:714.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.0%; Score 235.5; DB 8; Length 967;
Best Local Similarity 27.1%; Pred. No. 5.2e-11;
RESULT 816
ID ADS10576 standard; protein; 2428 AA.
DE Human therapeutic protein - SEQ ID 813.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 13.0%; Score 235.5; DB 8; Length 2428;
Best Local Similarity 26.9%; Pred. No. 1.8e-10;
RESULT 817
ID ADS2252 standard; protein; 2623 AA.
DE Human OCP protein #7.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.0%; Score 235.5; DB 8; Length 2623;
Best Local Similarity 26.9%; Pred. No. 2e-10;
RESULT 818
ID ADS10577 standard; protein; 2623 AA.
DE Human therapeutic protein - SEQ ID 814.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 13.0%; Score 235.5; DB 8; Length 2623;
Best Local Similarity 26.9%; Pred. No. 2e-10;
RESULT 819
ID ADN24073 standard; protein; 662 AA.
DE Bacterial polypeptide #6726.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.0%; Score 235; DB 8; Length 662;
Best Local Similarity 25.5%; Pred. No. 3.4e-11;
RESULT 820
ID ADD47171 standard; protein; 1040 AA.
DE Rat Protein AAA42201, SEQ ID NO 12864.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.0%; Score 234.5; DB 7; Length 1040;
Best Local Similarity 25.8%; Pred. No. 7e-11;
RESULT 821
ID ADR67266 standard; protein; 1100 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 12.9%; Score 233.5; DB 8; Length 1100;
Best Local Similarity 24.9%; Pred. No. 9.2e-11;
RESULT 822
ID ADH71816 standard; protein; 967 AA.
DE Human protein of the invention NOV29x SEQ ID NO:712.
PN WO2003102155-A2.

PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.9%; Score 232.5; DB 8; Length 967;
Best Local Similarity 26.8%; Pred. No. 9.4e-11;
RESULT 823
ID ADM23691 standard; protein; 2783 AA.
DE Bacterial polypeptide #6344.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.9%; Score 232.5; DB 8; Length 2783;
Best Local Similarity 23.5%; Pred. No. 4e-10;
RESULT 824
ID ABG69614 standard; protein; 2401 AA.
DE Human NOV12a protein.
PN WO200250277-A2.
PD 27-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 5; Length 2401;
Best Local Similarity 26.9%; Pred. No. 3.6e-10;
RESULT 825
ID ABG69619 standard; protein; 2447 AA.
DE Human NOV12f protein.
PN WO200250277-A2.
PD 27-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 5; Length 2447;
Best Local Similarity 26.9%; Pred. No. 3.7e-10;
RESULT 826
ID ADH3065 standard; protein; 2591 AA.
DE Human NOVX NOV12f protein.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCH/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 12.8%; Score 232; DB 7; Length 2591;
Best Local Similarity 26.9%; Pred. No. 4e-10;
RESULT 827
ID ADH71822 standard; protein; 2591 AA.
DE Human protein of the invention NOV29aa SEQ ID NO:718.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2591;
Best Local Similarity 26.9%; Pred. No. 4e-10;

PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 13.4%; Score 242; DB 5; Length 2587;
Best Local Similarity 27.0%; Pred. No. 5.5e-11;
RESULT 797
ID ADL02236 standard; protein; 2587 AA.
DE Human OCP protein #3.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 8; Length 2587;
Best Local Similarity 27.0%; Pred. No. 5.5e-11;
RESULT 798
ID ABG31323 standard; protein; 2589 AA.
DE Human OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 5; Length 2589;
Best Local Similarity 27.0%; Pred. No. 5.5e-11;
RESULT 799
ID ADL02244 standard; protein; 2589 AA.
DE Human OCP protein #5.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 8; Length 2589;
Best Local Similarity 27.0%; Pred. No. 5.5e-11;
RESULT 800
ID AAR92256 standard; protein; 582 AA.
DE Neural cell adhesion molecule splice variant.
PN WO9604396-A1.
PD 15-FEB-1996.
PA (SYST-) SYSTEMIX INC.
Query Match 13.4%; Score 241.5; DB 2; Length 582;
Best Local Similarity 24.4%; Pred. No. 7.9e-12;
RESULT 801
ID AAR92255 standard; protein; 761 AA.
DE Neural cell adhesion molecule.
PN WO9604396-A1.
PD 15-FEB-1996.
PA (SYST-) SYSTEMIX INC.
Query Match 13.4%; Score 241.5; DB 2; Length 761;
Best Local Similarity 24.4%; Pred. No. 1.1e-11;
RESULT 802
ID ADI24547 standard; protein; 837 AA.
DE Human modifier of CHK1 (MCHK) protein SEQ ID NO:97.
PN WO2004004785-A1.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 13.4%; Score 241.5; DB 8; Length 837;
Best Local Similarity 24.7%; Pred. No. 1.3e-11;
RESULT 803
ID ADJ76385 standard; protein; 1020 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1637.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 13.4%; Score 241.5; DB 8; Length 1020;
Best Local Similarity 24.3%; Pred. No. 1.7e-11;
RESULT 804
ID ABG07536 standard; protein; 891 AA.
DE Novel human diagnostic protein #7527.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.3%; Score 241; DB 4; Length 891;
Best Local Similarity 45.7%; Pred. No. 1.6e-11;
RESULT 805
ID ABP69251 standard; protein; 2173 AA.
DE Human polypeptide SEQ ID NO 1298.
PN WO200270539-A2.

PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 13.3%; Score 241; DB 5; Length 2173;
Best Local Similarity 26.7%; Pred. No. 5.3e-11;
RESULT 806
ID AAE00585 standard; protein; 793 AA.
DE Human nuclear cell adhesion molecule homologue, NCAM_c_1 protein.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 13.2%; Score 238.5; DB 4; Length 793;
Best Local Similarity 25.4%; Pred. No. 2.2e-11;
RESULT 807
ID AAE00584 standard; protein; 848 AA.
DE Human nuclear cell adhesion molecule homologue, NCAM_c_2 protein.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 13.2%; Score 238.5; DB 4; Length 848;
Best Local Similarity 25.4%; Pred. No. 2.4e-11;
RESULT 808
ID AAE00586 standard; protein; 891 AA.
DE Human nuclear cell adhesion molecule homologue, NCAM_d_2 protein.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 13.2%; Score 238.5; DB 4; Length 891;
Best Local Similarity 25.4%; Pred. No. 2.6e-11;
RESULT 809
ID AAE00583 standard; protein; 920 AA.
DE Human cell adhesion molecule homologue (CAM-H) protein #2.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 13.2%; Score 238.5; DB 4; Length 920;
Best Local Similarity 25.4%; Pred. No. 2.7e-11;
RESULT 810
ID AAE00582 standard; protein; 946 AA.
DE Human nuclear cell adhesion molecule homologue, NCAM_d_1 protein.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 13.2%; Score 238.5; DB 4; Length 946;
Best Local Similarity 25.4%; Pred. No. 2.8e-11;
RESULT 811
ID AAE00581 standard; protein; 1018 AA.
DE Human cell adhesion molecule homologue (CAM-H) protein #1.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 13.2%; Score 238.5; DB 4; Length 1018;
Best Local Similarity 25.4%; Pred. No. 3.1e-11;
RESULT 812
ID AAW05161 standard; protein; 73 AA.
DE Human LAMP residues 46-118.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 13.1%; Score 237; DB 2; Length 73;
Best Local Similarity 58.3%; Pred. No. 1.1e-12;
RESULT 813
ID AAW05162 standard; protein; 73 AA.
DE Rat LAMP residues 46-118.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDNJ) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 13.1%; Score 237; DB 2; Length 73;
Best Local Similarity 58.3%; Pred. No. 1.1e-12;
RESULT 814
ID ADR09877 standard; protein; 632 AA.
DE Human protein useful for treating neurological disease Seq 3383.
PN EP1447413-A2.
PD 18-AUG-2004.

RESULT 781
ID ADO28659 standard; protein; 1018 AA.
DE Human CONT protein SEQ ID NO:88.
FN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 13.6%; Score 246.5; DB 8; Length 1018;
Best Local Similarity 24.6%; Pred. No. 6.3e-12;
RESULT 782
ID ADF67246 standard; protein; 1018 AA.
DE Human F3/Contactin protein.
FN WO2004052389-A2.
PD 24-JUN-2004.
PA (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
PA (FORR/) FORREST G R.
Query Match 13.6%; Score 246.5; DB 8; Length 1018;
Best Local Similarity 24.6%; Pred. No. 6.3e-12;
RESULT 783
ID ADR66068 standard; protein; 1073 AA.
DE Human prostatic carcinoma derived protein SEQ ID 264 #1.
FN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 13.6%; Score 245.5; DB 8; Length 1073;
Best Local Similarity 26.4%; Pred. No. 8.2e-12;
RESULT 784
ID ADR66410 standard; protein; 1073 AA.
DE Human prostatic carcinoma derived protein SEQ ID 264 #2.
FN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 13.6%; Score 245.5; DB 8; Length 1073;
Best Local Similarity 26.4%; Pred. No. 8.2e-12;
RESULT 785
ID ADA54925 standard; protein; 512 AA.
DE Human protein, SEQ ID 2493.
FN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.5%; Score 244.5; DB 6; Length 512;
Best Local Similarity 27.8%; Pred. No. 3.6e-12;
RESULT 786
ID AA06485 standard; peptide; 1018 AA.
DE Rat contactin ligand for RPTPbeta.
FN WO9637776-A1.
PD 28-NOV-1996.
PA (SUGE-) SUGEN INC.
Query Match 13.5%; Score 243.5; DB 2; Length 1018;
Best Local Similarity 24.0%; Pred. No. 1.1e-11;
RESULT 787
ID ADE56173 standard; protein; 1021 AA.
DE Rat Protein O63198, SEQ ID NO 2022.
FN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.5%; Score 243.5; DB 7; Length 1021;
Best Local Similarity 24.0%; Pred. No. 1.1e-11;
RESULT 788
ID ABG03059 standard; protein; 792 AA.
DE Novel human diagnostic protein #3050.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.4%; Score 242.5; DB 4; Length 792;
Best Local Similarity 26.4%; Pred. No. 9.8e-12;
RESULT 789
ID ABG00258 standard; protein; 893 AA.
DE Novel human diagnostic protein #249.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.4%; Score 242.5; DB 4; Length 893;
Best Local Similarity 26.4%; Pred. No. 1.2e-11;
RESULT 790
ID ABG00611 standard; protein; 893 AA.
DE Novel human diagnostic protein #602.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.4%; Score 242.5; DB 4; Length 893;
Best Local Similarity 26.4%; Pred. No. 1.2e-11;
RESULT 791
ID ABG31317 standard; protein; 2586 AA.
DE Human 5+3 corrected OCP protein.
FN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 5; Length 2586;
Best Local Similarity 27.0%; Pred. No. 5.5e-11;
RESULT 792
ID ABG32891 standard; protein; 2586 AA.
DE Human osteoclast protein (OCP) #1.
FN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 13.4%; Score 242; DB 5; Length 2586;
Best Local Similarity 27.0%; Pred. No. 5.5e-11;
RESULT 793
ID ADL02231 standard; protein; 2586 AA.
DE Human OCP protein #1.
FN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 8; Length 2586;
Best Local Similarity 27.0%; Pred. No. 5.5e-11;
RESULT 794
ID ADL02234 standard; protein; 2586 AA.
DE Human OCP protein #2.
FN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 8; Length 2586;
Best Local Similarity 27.0%; Pred. No. 5.5e-11;
RESULT 795
ID AAB47935 standard; protein; 2587 AA.
DE Human OCP.
FN US2002020206-A1.
PD 21-FEB-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 13.4%; Score 242; DB 5; Length 2587;
Best Local Similarity 27.0%; Pred. No. 5.5e-11;
RESULT 796
ID ABG32896 standard; protein; 2587 AA.
DE Human osteoclast protein (OCP) #2.
FN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.

PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match 13.8%; Score 250; DB 8; Length 1315;
Best Local Similarity 27.7%; Pred. No. 4.4e-12;
RESULT 768
ID ADH72134 standard; protein; 1335 AA.
DE Human protein of the invention NOV46f SEQ ID NO:1030.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.8%; Score 250; DB 8; Length 1335;
Best Local Similarity 27.7%; Pred. No. 4.5e-12;
RESULT 769
ID ABUS2329 standard; protein; 1386 AA.
DE Human GPCR related protein NOV12a.
PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 13.8%; Score 250; DB 6; Length 1386;
Best Local Similarity 27.7%; Pred. No. 4.8e-12;
RESULT 770
ID ADL23993 standard; protein; 1386 AA.
DE Human NOVX polypeptide #19.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KERUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPVT/) SPYTEK K A.
PA (PART/) PARTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDGO F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENY S G.
PA (PADI/) PADIGARU M J.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (CASH/) CASHMAN S J.
PA (PENA/) PENA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.
PA (ZERR/) ZERRHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RASI/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match 13.8%; Score 250; DB 8; Length 1386;
Best Local Similarity 27.7%; Pred. No. 4.8e-12;
RESULT 771
ID ADD47172 standard; protein; 1040 AA.
DE Human Protein NP_005067, SEQ ID NO 12866.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO/) GEN HOSPITAL CORP.
PA (FARB/) BAYER AG.
Query Match 13.8%; Score 249.5; DB 7; Length 1040;
Best Local Similarity 26.1%; Pred. No. 3.6e-12;

RESULT 772
ID ADO28581 standard; protein; 1040 AA.
DE Human axonin-1 precursor (AXO1) protein SEQ ID NO:10.
PN WO200404178-A2.
PD 27-MAY-2004.
PA (GETH/) GENENTECH INC.
Query Match 13.8%; Score 249.5; DB 8; Length 1040;
Best Local Similarity 26.1%; Pred. No. 3.6e-12;
RESULT 773
ID ABO84729 standard; protein; 1040 AA.
DE Human cancer-associated protein HP22-025.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 13.8%; Score 249.5; DB 8; Length 1040;
Best Local Similarity 26.1%; Pred. No. 3.6e-12;
RESULT 774
ID ABO84728 standard; protein; 1040 AA.
DE Human cancer-associated protein HP22-025.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 13.8%; Score 249.5; DB 8; Length 1040;
Best Local Similarity 26.1%; Pred. No. 3.6e-12;
RESULT 775
ID ABG68882 standard; protein; 467 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33438.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE/) PE CORP NY.
Query Match 13.7%; Score 248; DB 4; Length 467;
Best Local Similarity 27.4%; Pred. No. 1.6e-12;
RESULT 776
ID ADJ68312 standard; protein; 1007 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID118.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 13.6%; Score 246.5; DB 7; Length 1007;
Best Local Similarity 24.6%; Pred. No. 6.2e-12;
RESULT 777
ID AAR63759 standard; protein; 1018 AA.
DE Human contactin (EMBL Accession #221488).
PN EP618293-A1.
PD 05-OCT-1994.
PA (BECT) BECTON DICKINSON CO.
Query Match 13.6%; Score 246.5; DB 2; Length 1018;
Best Local Similarity 24.6%; Pred. No. 6.3e-12;
RESULT 778
ID AAR87028 standard; protein; 1018 AA.
DE Human contactin.
PN WO9535373-A2.
PD 28-DEC-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 13.6%; Score 246.5; DB 2; Length 1018;
Best Local Similarity 24.6%; Pred. No. 6.3e-12;
RESULT 779
ID ADE71113 standard; protein; 1018 AA.
DE Contactin, SEQ ID 67.
PN WO2003070889-A2.
PD 28-AUG-2003.
PA (IDEC-) IDEC PHARM CORP.
Query Match 13.6%; Score 246.5; DB 7; Length 1018;
Best Local Similarity 24.6%; Pred. No. 6.3e-12;
RESULT 780
ID ADJ75696 standard; protein; 1018 AA.
DE Marker gene related amino acid sequence SEQ ID NO:948.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 13.6%; Score 246.5; DB 8; Length 1018;
Best Local Similarity 24.6%; Pred. No. 6.3e-12;

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Query Match      13.8%; Score 250; DB 8; Length 374;
Best Local Similarity 27.7%; Pred. No. 8e-13;
RESULT 753
ID AD047377 standard; protein; 440 AA.
DE Human neurotrophin-like protein-related protein SeqID12.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match      13.8%; Score 250; DB 8; Length 440;
Best Local Similarity 27.7%; Pred. No. 9.9e-13;
RESULT 754
ID ABB76022 standard; protein; 442 AA.
DE Neurotrophin-like polypeptide.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match      13.8%; Score 250; DB 4; Length 442;
Best Local Similarity 27.7%; Pred. No. 1e-12;
RESULT 755
ID ABB76017 standard; protein; 458 AA.
DE Neurotrophin-like polypeptide.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match      13.8%; Score 250; DB 4; Length 458;
Best Local Similarity 27.7%; Pred. No. 1e-12;
RESULT 756
ID AD047369 standard; protein; 458 AA.
DE Human neurotrophin-like protein SeqID4.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match      13.8%; Score 250; DB 8; Length 458;
Best Local Similarity 27.7%; Pred. No. 1e-12;
RESULT 757
ID ADS10607 standard; protein; 458 AA.
DE Human therapeutic protein - SEQ ID 844.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match      13.8%; Score 250; DB 8; Length 458;
Best Local Similarity 27.7%; Pred. No. 1e-12;
RESULT 758
ID AD047385 standard; protein; 880 AA.
DE Human neurotrophin-like protein-related protein SeqID13.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match      13.8%; Score 250; DB 8; Length 880;
Best Local Similarity 27.7%; Pred. No. 2.6e-12;
RESULT 759
ID AAO30844 standard; protein; 886 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-34.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match      13.8%; Score 250; DB 7; Length 886;
Best Local Similarity 27.7%; Pred. No. 2.6e-12;
RESULT 760
ID AD047396 standard; protein; 955 AA.
DE Human neurotrophin-like protein-related MAM domain GPIM protein SeqID31.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match      13.8%; Score 250; DB 8; Length 955;
Best Local Similarity 27.7%; Pred. No. 2.9e-12;
RESULT 761
ID AD047383 standard; protein; 955 AA.
DE Human neurotrophin-like protein SeqID18.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match      13.8%; Score 250; DB 8; Length 955;
Best Local Similarity 27.7%; Pred. No. 2.9e-12;
RESULT 762
ID ADS10608 standard; protein; 955 AA.
DE Human therapeutic protein - SEQ ID 845.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match      13.8%; Score 250; DB 8; Length 955;
Best Local Similarity 27.7%; Pred. No. 2.9e-12;
RESULT 763
ID ADS11107 standard; protein; 970 AA.
DE Human therapeutic protein - SEQ ID 1344.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match      13.8%; Score 250; DB 8; Length 970;
Best Local Similarity 27.7%; Pred. No. 2.9e-12;
RESULT 764
ID ABG12100 standard; protein; 1219 AA.
DE Novel human diagnostic protein #12091.
PN WO200175057-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match      13.8%; Score 250; DB 4; Length 1219;
Best Local Similarity 27.7%; Pred. No. 4e-12;
RESULT 765
ID ABU52336 standard; protein; 1315 AA.
DE Human GPCR related protein NOV13a.
PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match      13.8%; Score 250; DB 6; Length 1315;
Best Local Similarity 27.7%; Pred. No. 4.4e-12;
RESULT 766
ID ADH72138 standard; protein; 1315 AA.
DE Human protein of the invention NOV46h SEQ ID NO:1034.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match      13.8%; Score 250; DB 8; Length 1315;
Best Local Similarity 27.7%; Pred. No. 4.4e-12;
RESULT 767
ID ADL24007 standard; protein; 1315 AA.
DE Human NOVX polypeptide #26.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KEKUDA R.
PA (TCHU/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATT/) PATURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENY S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAPIER R J.
PA (MILL/) MILLER C E.
PA (CASM/) CASMAN S J.
PA (PENA/) PENA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RAST/) RASTELLI L.

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PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.1%; Score 254.5; DB 8; Length 5175;
Best Local Similarity 29.3%; Pred. No. 1.2e-11;
RESULT 736
ID ADN24207 standard; protein; 5198 AA.
DE Bacterial polypeptide #6860.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.1%; Score 254.5; DB 8; Length 5198;
Best Local Similarity 29.3%; Pred. No. 1.2e-11;
RESULT 737
ID ADN24205 standard; protein; 5198 AA.
DE Bacterial polypeptide #6858.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.1%; Score 254.5; DB 8; Length 5198;
Best Local Similarity 29.3%; Pred. No. 1.2e-11;
RESULT 738
ID ADM74177 standard; protein; 306 AA.
DE Human NOV3D protein sequence SeqID16.
PN WO2004015079-A2.
PD 19-FEB-2004.
PA (CURA-) CURAGEN CORP.
Query Match 14.0%; Score 253.5; DB 8; Length 306;
Best Local Similarity 27.1%; Pred. No. 3e-13;
RESULT 739
ID ABG66677 standard; protein; 404 AA.
DE Human novel polypeptide #12.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 14.0%; Score 253.5; DB 5; Length 404;
Best Local Similarity 27.1%; Pred. No. 4.4e-13;
RESULT 740
ID ABJ20221 standard; protein; 404 AA.
DE Human IG gene related protein SEQ ID No 44.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 14.0%; Score 253.5; DB 6; Length 404;
Best Local Similarity 27.1%; Pred. No. 4.4e-13;
RESULT 741
ID ADF66751 standard; protein; 404 AA.
DE Novel human protein NOV12.
PN US2003199103-A1.
PD 23-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.0%; Score 253.5; DB 8; Length 404;
Best Local Similarity 27.1%; Pred. No. 4.4e-13;
RESULT 742
ID ADI19788 standard; protein; 404 AA.
DE Human NOV12 protein.
PN US2004002134-A1.
PD 01-JAN-2004.
PA (CURA-) CURAGEN CORP.
Query Match 14.0%; Score 253.5; DB 8; Length 404;
Best Local Similarity 27.1%; Pred. No. 4.4e-13;
RESULT 743
ID ADO60261 standard; protein; 404 AA.
DE Human NOV12 protein.
PN US2003134430-A1.
PD 17-JUL-2003.

PA (CURA-) CURAGEN CORP.
Query Match 14.0%; Score 253.5; DB 8; Length 404;
Best Local Similarity 27.1%; Pred. No. 4.4e-13;
RESULT 744
ID ADO47378 standard; protein; 568 AA.
DE Human neurotrophin-like protein-related protein SeqID13.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 14.0%; Score 253; DB 8; Length 568;
Best Local Similarity 27.4%; Pred. No. 7.8e-13;
RESULT 745
ID ABB76023 standard; protein; 570 AA.
DE Neurotrophin-like polypeptide.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.0%; Score 253; DB 4; Length 570;
Best Local Similarity 27.4%; Pred. No. 7.8e-13;
RESULT 746
ID ABB76018 standard; protein; 586 AA.
DE Neurotrophin-like polypeptide splice variant.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.0%; Score 253; DB 4; Length 586;
Best Local Similarity 27.4%; Pred. No. 8.1e-13;
RESULT 747
ID ADO47372 standard; protein; 586 AA.
DE Human neurotrophin-like protein SeqID7.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 14.0%; Score 253; DB 8; Length 586;
Best Local Similarity 27.4%; Pred. No. 8.1e-13;
RESULT 748
ID ABO23244 standard; protein; 404 AA.
DE Human breast tumour associated protein 47-like polypeptide NOV12.
PN US2003027158-A1.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.9%; Score 251.5; DB 6; Length 404;
Best Local Similarity 27.1%; Pred. No. 6.6e-13;
RESULT 749
ID AAB61142 standard; protein; 404 AA.
DE Human NOV12 protein.
PN WO200075321-A2.
PD 14-DEC-2000.
PA (CURA-) CURAGEN CORP.
Query Match 13.9%; Score 250.5; DB 4; Length 404;
Best Local Similarity 27.1%; Pred. No. 8e-13;
RESULT 750
ID ABB61502 standard; protein; 895 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11298.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.9%; Score 250.5; DB 4; Length 885;
Best Local Similarity 26.5%; Pred. No. 2.3e-12;
RESULT 751
ID ABB76016 standard; protein; 374 AA.
DE Neurotrophin-like polypeptide.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.8%; Score 250; DB 4; Length 374;
Best Local Similarity 27.7%; Pred. No. 8e-13;
RESULT 752
ID ADO47381 standard; protein; 374 AA.
DE Human neurotrophin-like protein-related protein SeqID16.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.

PA (HYSE-) HYSEQ INC.
Query Match 14.9%; Score 268.5; DB 6; Length 1498;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 719
ID AAG02771 standard; protein; 58 AA.
DE Human secreted protein, SEQ ID NO: 6852.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 14.8%; Score 267; DB 3; Length 58;
Best Local Similarity 86.2%; Pred. No. 2.1e-15;
RESULT 720
ID ABB37902 standard; protein; 142 AA.
DE Human secretory polypeptide (SPTM) 154.
PN WO20020756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 14.6%; Score 263; DB 5; Length 142;
Best Local Similarity 44.1%; Pred. No. 1.6e-14;
RESULT 721
ID AAY13563 standard; protein; 1395 AA.
DE Drosophila Robo 1 polypeptide.
PN WO9925833-A1.
PD 27-MAY-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 14.5%; Score 261; DB 2; Length 1395;
Best Local Similarity 26.1%; Pred. No. 5.4e-13;
RESULT 722
ID AAY08401 standard; protein; 1395 AA.
DE Drosophila sp. ROBO1 protein.
PN WO9920764-A1.
PD 29-APR-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 14.5%; Score 261; DB 2; Length 1395;
Best Local Similarity 26.1%; Pred. No. 5.4e-13;
RESULT 723
ID ADB85335 standard; protein; 1395 AA.
DE Fruitfly nerve cell growth modulator SLIT-1-associated sequence #1.
PN US2003170727-A1.
PD 11-SEP-2003.
PA (GOOD/) GOODMAN C S.
PA (KIDD/) KIDD T.
PA (BROS/) BROSE K.
PA (TESS/) TESSIER-LAVIGNE M.
Query Match 14.5%; Score 261; DB 7; Length 1395;
Best Local Similarity 26.1%; Pred. No. 5.4e-13;
RESULT 724
ID ABB62052 standard; protein; 496 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12948.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.4%; Score 260.5; DB 4; Length 496;
Best Local Similarity 26.2%; Pred. No. 1.5e-13;
RESULT 725
ID ABB68257 standard; protein; 1395 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31563.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.4%; Score 260; DB 4; Length 1395;
Best Local Similarity 26.1%; Pred. No. 6.6e-13;
RESULT 726
ID AAY53666 standard; protein; 4412 AA.
DE Sequence gi/1017427/emb/CNA62189 from an alignment with protein 608.
PN WO9960164-A1.
PD 25-NOV-1999.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 14.3%; Score 259; DB 3; Length 4412;
Best Local Similarity 29.6%; Pred. No. 3.9e-12;
RESULT 727
ID ABG74786 standard; protein; 31267 AA.
DE Human RGS11 protein.

PN WO2002103355-A1.
PD 27-DEC-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 14.3%; Score 259; DB 6; Length 31267;
Best Local Similarity 29.6%; Pred. No. 5.7e-11;
RESULT 728
ID ADQ89964 standard; protein; 34350 AA.
DE Antagonist of cell cycle progression polypeptide #197.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 14.3%; Score 259; DB 8; Length 34350;
Best Local Similarity 29.6%; Pred. No. 6.4e-11;
RESULT 729
ID ADM74171 standard; protein; 381 AA.
DE Human NOV3A protein sequence SeqID10.
PN WO2004015079-A2.
PD 19-FEB-2004.
PA (CURA-) CURAGEN CORP.
Query Match 14.3%; Score 258.5; DB 8; Length 381;
Best Local Similarity 27.4%; Pred. No. 1.5e-13;
RESULT 730
ID ADM56387 standard; protein; 404 AA.
DE Human cell adhesion molecule NOV12.
PN US2003082554-A1.
PD 01-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.2%; Score 256.5; DB 7; Length 404;
Best Local Similarity 27.4%; Pred. No. 2.4e-13;
RESULT 731
ID AAY33741 standard; protein; 444 AA.
DE Beta-secretase.
PN US9942400-A.
PD 24-AUG-1999.
PA (ELAN-) ELAN PHARM INC.
Query Match 14.2%; Score 256; DB 2; Length 444;
Best Local Similarity 26.7%; Pred. No. 3.1e-13;
RESULT 732
ID AAB47251 standard; protein; 444 AA.
DE Beta-secretase.
PN US6221645-B1.
PD 24-APR-2001.
PA (ELAN-) ELAN PHARM INC.
Query Match 14.2%; Score 256; DB 4; Length 444;
Best Local Similarity 26.7%; Pred. No. 3.1e-13;
RESULT 733
ID ABB63920 standard; protein; 359 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18552.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.1%; Score 255; DB 4; Length 359;
Best Local Similarity 24.9%; Pred. No. 2.8e-13;
RESULT 734
ID ADN24208 standard; protein; 5175 AA.
DE Bacterial polypeptide #6861.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.1%; Score 254.5; DB 8; Length 5175;
Best Local Similarity 29.3%; Pred. No. 1.2e-11;
RESULT 735
ID ADN24206 standard; protein; 5175 AA.
DE Bacterial polypeptide #6859.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.9%; Score 269; DB 4; Length 152;
Best Local Similarity 42.3%; Pred. No. 5.3e-15;
RESULT 703
ID ADB31647 standard; protein; 152 AA.
DE Human novel protein SEQ ID NO 168.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.9%; Score 269; DB 7; Length 152;
Best Local Similarity 42.3%; Pred. No. 5.3e-15;
RESULT 704
ID ADR66889 standard; protein; 1469 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 187 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.9%; Score 268.5; DB 8; Length 1469;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 705
ID ADR65991 standard; protein; 1469 AA.
DE Human prostatic carcinoma derived protein SEQ ID 187 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.9%; Score 268.5; DB 8; Length 1469;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 706
ID ADL35717 standard; protein; 1479 AA.
DE Human peroxidasin-melanoma antigen-related protein.
PN WO2004019893-A2.
PD 11-MAR-2004.
PA (RICE-) RIGEL PHARM INC.
Query Match 14.9%; Score 268.5; DB 8; Length 1479;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 707
ID AAW81030 standard; protein; 1496 AA.
DE Melanoma associated antigen MG50.
PN WO955513-A1.
PD 10-DEC-1998.
PA (REG-) UNIV CALIFORNIA.
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
Query Match 14.9%; Score 268.5; DB 2; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 708
ID AAY70469 standard; protein; 1496 AA.
DE Human p53 target molecule, PRG2 protein.
PN WO200012526-A1.
PD 09-MAR-2000.
PA (UYPR-) UNIV PRINCETON.
Query Match 14.9%; Score 268.5; DB 3; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 709
ID ABU03498 standard; protein; 1496 AA.
DE Angiogenesis-associated human protein sequence #43.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 14.9%; Score 268.5; DB 6; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 710
ID ADD89024 standard; protein; 1496 AA.
DE TAT264.
PN WO2003057160-A2.

PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 14.9%; Score 268.5; DB 7; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 711
ID ADF28706 standard; protein; 1496 AA.
DE Human peroxidasin-like MG50 protein - SEQ ID 616.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 14.9%; Score 268.5; DB 7; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 712
ID ADQ18902 standard; protein; 1496 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1721.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 713
ID ADQ89920 standard; protein; 1496 AA.
DE Antagonist of cell cycle progression polypeptide #175.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 714
ID ADQ89914 standard; protein; 1496 AA.
DE Antagonist of cell cycle progression polypeptide #172.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 715
ID ADR66092 standard; protein; 1496 AA.
DE Human prostatic carcinoma derived protein SEQ ID 288 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 716
ID ADR66434 standard; protein; 1496 AA.
DE Human prostatic carcinoma derived protein SEQ ID 288 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 717
ID ABB11587 standard; peptide; 1498 AA.
DE Human peroxidasin homologue, SEQ ID NO:1957.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.9%; Score 268.5; DB 4; Length 1498;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 718
ID ABO00762 standard; protein; 1498 AA.
DE Polypeptide encoded by novel human contig #13.
PN WO2003023013-A2.
PD 20-MAR-2003.

DE Drosophila melanogaster polypeptide SEQ ID NO 15924.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PKE) PE CORP NY.
Query Match 15.8%; Score 284.5; DB 4; Length 467;
Best Local Similarity 26.1%; Pred. No. 1.1e-15;
RESULT 688
ID AD563330 standard; protein; 858 AA.
DE Rat Protein P13596, SEQ ID NO 9269.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 15.4%; Score 277.5; DB 7; Length 858;
Best Local Similarity 25.5%; Pred. No. 1.1e-14;
RESULT 689
ID ADA55624 standard; protein; 733 AA.
DE Human protein, SEQ ID 3192.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.3%; Score 276; DB 6; Length 733;
Best Local Similarity 25.7%; Pred. No. 1.1e-14;
RESULT 690
ID AD563332 standard; protein; 761 AA.
DE Human Protein P13592, SEQ ID NO 9270.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 15.3%; Score 276; DB 7; Length 761;
Best Local Similarity 25.7%; Pred. No. 1.2e-14;
RESULT 691
ID AAY88565 standard; protein; 848 AA.
DE Human NCAM 140KD isoform precursor amino acid sequence.
PN WO200018801-A2.
PD 06-APR-2000.
PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.
PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.
Query Match 15.3%; Score 276; DB 3; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.4e-14;
RESULT 692
ID AA817222 standard; protein; 848 AA.
DE Human 140kd NCAM isoform protein.
PN WO200196364-A2.
PD 20-DEC-2001.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
PA (UNLO) KINGS COLLEGE LONDON.
Query Match 15.3%; Score 276; DB 5; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.4e-14;
RESULT 693
ID AD124546 standard; protein; 848 AA.
DE Human modifier of Chk1 (MCHK) protein SEQ ID NO:96.
PN WO2004004785-A1.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 15.3%; Score 276; DB 8; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.4e-14;
RESULT 694
ID ADF28603 standard; protein; 853 AA.
DE Bovine NCAM-140 protein - SED ID 513.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.

Query Match 15.3%; Score 275.5; DB 7; Length 853;
Best Local Similarity 25.5%; Pred. No. 1.6e-14;
RESULT 695
ID ADJ36019 standard; protein; 90 AA.
DE Human NOVX-related polypeptide #17.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 15.2%; Score 275; DB 7; Length 90;
Best Local Similarity 61.8%; Pred. No. 7.9e-16;
RESULT 696
ID ADD25619 standard; protein; 848 AA.
DE Binding domain-immunoglobulin fusion protein-associated protein #87.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENE-CRAFT INC.
Query Match 15.2%; Score 275; DB 7; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.7e-14;
RESULT 697
ID AAE37177 standard; protein; 1477 AA.
DE Human LRRCAPS protein #2.
PN WO2003035831-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 15.2%; Score 274; DB 6; Length 1477;
Best Local Similarity 29.2%; Pred. No. 4.4e-14;
RESULT 698
ID ADH48824 standard; protein; 1356 AA.
DE NOV45B protein sequence, SEQ ID 108.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 15.1%; Score 273.5; DB 5; Length 1356;
Best Local Similarity 29.6%; Pred. No. 4.4e-14;
RESULT 699
ID ADH48822 standard; protein; 1426 AA.
DE NOV45A protein sequence, SEQ ID 106.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 15.0%; Score 271.5; DB 5; Length 1426;
Best Local Similarity 29.6%; Pred. No. 6.9e-14;
RESULT 700
ID AAO30845 standard; protein; 859 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-35.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.0%; Score 271; DB 7; Length 859;
Best Local Similarity 24.8%; Pred. No. 3.8e-14;
RESULT 701
ID ABB68566 standard; protein; 729 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 32490.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PKE) PE CORP NY.
Query Match 15.0%; Score 270; DB 4; Length 729;
Best Local Similarity 26.7%; Pred. No. 3.7e-14;
RESULT 702
ID AAU18023 standard; protein; 152 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 168.
PN WO200155315-A2.

PA (SPYT/) SPYTEK K A.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERR/) ZERHUSEN B D.
Query Match 16.0%; Score 288.5; DB 8; Length 961;
Best Local Similarity 30.5%; Pred. No. 1.4e-15;
RESULT 678
ID ABG03933 standard; protein; 1240 AA.
DE Novel human diagnostic protein #3924.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 16.0%; Score 288.5; DB 4; Length 1240;
Best Local Similarity 31.1%; Pred. No. 2e-15;
RESULT 679
ID AAB4771 standard; protein; 1336 AA.
DE Human thrombospondin protein, BTL.012.
PN WO200174852-A2.
PD 11-OCT-2001.
PA (FARB) BAYER CORP.
Query Match 16.0%; Score 288.5; DB 5; Length 1336;
Best Local Similarity 31.1%; Pred. No. 2.2e-15;
RESULT 680
ID ABU12084 standard; protein; 1902 AA.
DE Human NOV25c CG56914-03 protein SEQ ID 88.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.0%; Score 288.5; DB 6; Length 1902;
Best Local Similarity 31.1%; Pred. No. 3.5e-15;
RESULT 681
ID ADH72108 standard; protein; 1902 AA.
DE Human protein of the invention NOV43d SEQ ID NO:1004.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.0%; Score 288.5; DB 8; Length 1902;
Best Local Similarity 31.1%; Pred. No. 3.5e-15;
RESULT 682
ID ADE16058 standard; protein; 1953 AA.
DE G-coupled protein receptor related polypeptide, SEQ ID NO 88.
PN WO200283841-A2.
PD 24-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.0%; Score 288.5; DB 7; Length 1953;
Best Local Similarity 31.1%; Pred. No. 3.6e-15;
RESULT 683
ID ADL93997 standard; protein; 1953 AA.
DE Human G-coupled protein receptor-related protein #44.
PN US2004006205-A1.
PD 08-JAN-2004.
PA (LILL/) LI L.
PA (GERL/) GERLACH V.
PA (LIUX/) LIU X.
PA (MILL/) MILLER C E.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERHUSEN B D.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (ZHON/) ZHONG H.
PA (SMIT/) SMITHSON G.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOGF L.
PA (VOSS/) VOSS E Z.
PA (VERN/) VERNET C A.
PA (MACD/) MACDOUGALL J R.
PA (RAST/) RASTELLI L.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (MEZE/) MEZES P S.
PA (FURT/) FURIAK K.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.

PA (MALY/) MALYANKAR U M.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
Query Match 16.0%; Score 288.5; DB 8; Length 1953;
Best Local Similarity 31.1%; Pred. No. 3.6e-15;
RESULT 684
ID ADJ83136 standard; protein; 3645 AA.
DE Human hemocentrin protein - SEQ ID 127.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SEK/) SEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOGF L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 16.0%; Score 288.5; DB 7; Length 3645;
Best Local Similarity 31.1%; Pred. No. 8.6e-15;
RESULT 685
ID ABP60991 standard; protein; 5635 AA.
DE Novel human protein. SEQ ID 78.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 16.0%; Score 288.5; DB 5; Length 5635;
Best Local Similarity 31.1%; Pred. No. 1.6e-14;
RESULT 686
ID ADG39841 standard; protein; 1708 AA.
DE Protein similar to human NOV9 #2.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 15.9%; Score 287.5; DB 7; Length 1708;
Best Local Similarity 31.1%; Pred. No. 3.7e-15;
RESULT 687
ID ABB63044 standard; protein; 467 AA.

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Best Local Similarity 31.1%; Pred. No. 1e-14;
RESULT 669
ID ADP73129 standard; protein; 5636 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P29.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE//) GENE S.
PA (ALMS//) AL M S.
Query Match 16.1%; Score 290.5; DB 8; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1e-14;
RESULT 670
ID ADG39844 standard; protein; 1708 AA.
DE Protein similar to human NOV9 #5.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA//) PENA C E A.
PA (GUOX//) GUO X.
PA (SHIM//) SHIMKETS R A.
PA (PADI//) PADIGARU M.
PA (KEKU//) KEKUDA R.
PA (SPVT//) SPYTEK K A.
PA (MEHR//) MEHRABAN F.
PA (TOPP//) TOPPER J N.
PA (MALY//) MALYANKAR U M.
PA (WASS//) WASSERMAN S M.
PA (EDIN//) EDINGER S R.
PA (SMIT//) SMITHSON G.
PA (GUNT//) GUNTHER E.
PA (KOMU//) KOMUVES L.
Query Match 16.0%; Score 289.5; DB 7; Length 1708;
Best Local Similarity 29.8%; Pred. No. 2.5e-15;
RESULT 671
ID ADG39840 standard; protein; 1708 AA.
DE Protein similar to human NOV9 #1.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA//) PENA C E A.
PA (GUOX//) GUO X.
PA (SHIM//) SHIMKETS R A.
PA (PADI//) PADIGARU M.
PA (KEKU//) KEKUDA R.
PA (SPYT//) SPYTEK K A.
PA (MEHR//) MEHRABAN F.
PA (TOPP//) TOPPER J N.
PA (MALY//) MALYANKAR U M.
PA (WASS//) WASSERMAN S M.
PA (EDIN//) EDINGER S R.
PA (SMIT//) SMITHSON G.
PA (GUNT//) GUNTHER E.
PA (KOMU//) KOMUVES L.
Query Match 16.0%; Score 288.5; DB 8; Length 707;
Best Local Similarity 31.1%; Pred. No. 9.1e-16;
RESULT 672
ID ABU69134 standard; protein; 707 AA.
DE Human NOVX polypeptide #9.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.0%; Score 288.5; DB 6; Length 707;
Best Local Similarity 31.1%; Pred. No. 9.1e-16;
RESULT 673
ID ADH72102 standard; protein; 707 AA.
DE Human protein of the invention NOV43a SEQ ID NO:998.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.0%; Score 288.5; DB 8; Length 707;
Best Local Similarity 31.1%; Pred. No. 9.1e-16;
RESULT 674
ID ADO08271 standard; protein; 707 AA.
DE Human NOVX polypeptide #9.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO//) ALSOBROOK J P.
PA (ANDE//) ANDERSON D W.
PA (BOLD//) BOLDOG F L.
PA (BURG//) BURGESS C E.
PA (CASM//) CASMAN S J.
PA (CHAP//) CHAPOVAL A.
PA (EDIN//) EDINGER S R.
PA (GERL//) GERLACH V.
PA (GORM//) GORMAN L.
PA (GUNT//) GUNTHER E.
PA (GUOX//) GUO X S.
PA (KEKU//) KEKUDA R.
PA (LEPL//) LEPLEY D M.
PA (LILL//) LI L.
PA (LIUX//) LIU X.
PA (MALY//) MALYANKAR U M.
PA (MILL//) MILLER C E.
PA (MILL//) MILLET I.
PA (PADI//) PADIGARU M.
PA (PATT//) PATTURAJAN M.
PA (PENA//) PENA C E A.
PA (RIEG//) RIEGER D K.
PA (SHEN//) SHENOY S G.
PA (SHIM//) SHIMKETS R A.
PA (SPYT//) SPYTEK K A.
PA (TAUP//) TAUPIER R J.
PA (VERN//) VERNET C A M.
PA (VOSS//) VOSS E Z.
PA (ZERH//) ZERHUSEN B D.
Query Match 16.0%; Score 288.5; DB 8; Length 707;
Best Local Similarity 31.1%; Pred. No. 9.1e-16;
RESULT 675
ID ADH72104 standard; protein; 712 AA.
DE Human protein of the invention NOV43b SEQ ID NO:1000.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.0%; Score 288.5; DB 8; Length 712;
Best Local Similarity 31.1%; Pred. No. 9.2e-16;
RESULT 676
ID ABU99129 standard; protein; 961 AA.
DE Novel human GPCR related protein NOV9b.
PN WO200299116-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.0%; Score 288.5; DB 6; Length 961;
Best Local Similarity 30.5%; Pred. No. 1.4e-15;
RESULT 677
ID ADM93823 standard; protein; 961 AA.
DE Human NOV protein #21.
PN US2004009480-A1.
PD 15-JAN-2004.
PA (ANDE//) ANDERSON D W.
PA (BAUM//) BAUMGARTNER J C.
PA (BOLD//) BOLDOG F L.
PA (CASM//) CASMAN S J.
PA (EDIN//) EDINGER S R.
PA (GANG//) GANGOLLI E A.
PA (GERL//) GERLACH V.
PA (GORM//) GORMAN L.
PA (GUOX//) GUO X S.
PA (HJAL//) HJALT T.
PA (KEKU//) KEKUDA R.
PA (LILL//) LI L.
PA (MACD//) MACDOUGALL J R.
PA (MALY//) MALYANKAR U M.
PA (MILL//) MILLET I.
PA (PADI//) PADIGARU M.
PA (PATT//) PATTURAJAN M.
PA (PENA//) PENA C E A.
PA (RAST//) RASTELLI L.
PA (SHIM//) SHIMKETS R A.
PA (STON//) STONE D J.

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RESULT 658
ID ABU12083 standard; protein; 2572 AA.
DE Human NOV25b CG93858-02 protein SEQ ID 86.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 6; Length 2572;
Best Local Similarity 29.8%; Pred. No. 3.6e-15;
RESULT 659
ID ADK60225 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR283687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 2673;
Best Local Similarity 29.8%; Pred. No. 3.8e-15;
RESULT 660
ID ADK60526 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR283686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 2673;
Best Local Similarity 29.8%; Pred. No. 3.8e-15;
RESULT 661
ID ADP73149 standard; protein; 2673 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P52.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match 16.1%; Score 290.5; DB 8; Length 2673;
Best Local Similarity 29.8%; Pred. No. 3.8e-15;
RESULT 662
ID ABU69135 standard; protein; 4495 AA.
DE Human NOVX polypeptide #10.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 6; Length 4495;
Best Local Similarity 29.8%; Pred. No. 7.7e-15;
RESULT 663
ID ADH72106 standard; protein; 4495 AA.
DE Human protein of the invention NOV43c SEQ ID NO:1002.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 8; Length 4495;
Best Local Similarity 29.8%; Pred. No. 7.7e-15;
RESULT 664
ID ADO08273 standard; protein; 4495 AA.
DE Human NOVX polypeptide #10.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALI/) MADIYANKAR U M.
PA (MILL/) MILLER C E.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS B Z.
PA (ZERH/) ZERHUSEN B D.
Query Match 16.1%; Score 290.5; DB 8; Length 4495;
Best Local Similarity 29.8%; Pred. No. 7.7e-15;
RESULT 665
ID ADJ70089 standard; protein; 5636 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1895.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 16.1%; Score 290.5; DB 7; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1e-14;
RESULT 666
ID ADJ83137 standard; protein; 5636 AA.
DE Human hemocentin protein - SEQ ID 128.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 16.1%; Score 290.5; DB 7; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1e-14;
RESULT 667
ID ADK60205 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR283687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1e-14;
RESULT 668
ID ADK60506 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR283686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 5636;
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Query Match 37.7%; Score 681.5; DB 5; Length 351;
Best Local Similarity 50.7%; Pred. No. 4.4e-50;
RESULT 640
ID ABG13848 standard; protein; 141 AA.
DE Novel human diagnostic protein #13839.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 33.4%; Score 603; DB 4; Length 141;
Best Local Similarity 86.6%; Pred. No. 7.5e-44;
RESULT 641
ID AAE30271 standard; protein; 294 AA.
DE Human LP319b protein variant #2.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 33.4%; Score 603; DB 6; Length 294;
Best Local Similarity 45.0%; Pred. No. 2e-43;
RESULT 642
ID AAE30270 standard; protein; 286 AA.
DE Human LP319b protein variant #1.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 33.2%; Score 600; DB 6; Length 286;
Best Local Similarity 45.0%; Pred. No. 3.6e-43;
RESULT 643
ID ADP29917 standard; protein; 222 AA.
DE Human secreted protein SEQ ID #684.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 33.2%; Score 599.5; DB 8; Length 222;
Best Local Similarity 54.0%; Pred. No. 2.8e-43;
RESULT 644
ID ABG13847 standard; protein; 130 AA.
DE Novel human diagnostic protein #13838.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 31.5%; Score 569.5; DB 4; Length 130;
Best Local Similarity 88.9%; Pred. No. 5.2e-41;
RESULT 645
ID AAE30269 standard; protein; 234 AA.
DE Human LP319b protein mature sequence #2.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 29.2%; Score 527; DB 6; Length 234;
Best Local Similarity 53.2%; Pred. No. 5.4e-37;
RESULT 646
ID AAE29927 standard; protein; 256 AA.
DE Human LP319b protein.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 29.2%; Score 527; DB 6; Length 256;
Best Local Similarity 53.2%; Pred. No. 6.1e-37;
RESULT 647
ID ABG13816 standard; protein; 872 AA.
DE Novel human diagnostic protein #13807.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 29.1%; Score 525.5; DB 4; Length 872;
Best Local Similarity 43.4%; Pred. No. 4.4e-36;
RESULT 648
ID ADS08994 standard; protein; 872 AA.
DE Novel protein-related contig polypeptide sequence #60.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 29.1%; Score 525.5; DB 7; Length 872;

Best Local Similarity 43.4%; Pred. No. 4.4e-36;
RESULT 649
ID AAE30268 standard; protein; 226 AA.
DE Human LP319b protein mature sequence #1.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 28.0%; Score 505; DB 6; Length 226;
Best Local Similarity 53.0%; Pred. No. 4e-35;
RESULT 650
ID AAE30264 standard; protein; 211 AA.
DE Human LP319a protein mature sequence #1.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 26.1%; Score 472; DB 6; Length 211;
Best Local Similarity 54.1%; Pred. No. 2.6e-32;
RESULT 651
ID AAE30265 standard; protein; 222 AA.
DE Human LP319a protein mature sequence #2.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 26.1%; Score 472; DB 6; Length 222;
Best Local Similarity 54.1%; Pred. No. 2.8e-32;
RESULT 652
ID AAE29926 standard; protein; 241 AA.
DE Human LP319a protein.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 26.1%; Score 472; DB 6; Length 241;
Best Local Similarity 54.1%; Pred. No. 3.1e-32;
RESULT 653
ID ABB69485 standard; protein; 413 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35247.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 18.7%; Score 338.5; DB 4; Length 413;
Best Local Similarity 28.0%; Pred. No. 2.1e-20;
RESULT 654
ID ABB65642 standard; protein; 315 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23718.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 18.4%; Score 333; DB 4; Length 315;
Best Local Similarity 31.9%; Pred. No. 4.4e-20;
RESULT 655
ID ABB62574 standard; protein; 545 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14514.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 16.9%; Score 306; DB 4; Length 545;
Best Local Similarity 28.9%; Pred. No. 2e-17;
RESULT 656
ID ABB58947 standard; protein; 333 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3633.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 16.5%; Score 297.5; DB 4; Length 333;
Best Local Similarity 29.7%; Pred. No. 5.4e-17;
RESULT 657
ID ADS10483 standard; protein; 2537 AA.
DE Human therapeutic protein - SEQ ID 720.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 16.1%; Score 290.5; DB 8; Length 2537;
Best Local Similarity 29.8%; Pred. No. 3.5e-15;

PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 40.2%; Score 726; DB 5; Length 336;
Best Local Similarity 50.5%; Pred. No. 6e-54;
RESULT 633
ID ABG94639 standard; protein; 336 AA.
DE Human NOV5d protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 39.9%; Score 721; DB 5; Length 336;
Best Local Similarity 50.5%; Pred. No. 1.6e-53;
RESULT 634
ID ADH71408 standard; protein; 336 AA.
DE Human protein of the invention NOV111 SEQ ID NO:304.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.9%; Score 721; DB 8; Length 336;
Best Local Similarity 50.5%; Pred. No. 1.6e-53;
RESULT 635
ID ABB10253 standard; protein; 281 AA.
DE Human CDNA SEQ ID NO: 561.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.9%; Score 720.5; DB 4; Length 281;
Best Local Similarity 50.4%; Pred. No. 1.4e-53;
RESULT 636
ID ABP66840 standard; protein; 281 AA.
DE Human polypeptide SEQ ID NO 561.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA-) BARASH S C.
Query Match 39.9%; Score 720.5; DB 5; Length 281;
Best Local Similarity 50.4%; Pred. No. 1.4e-53;
RESULT 637
ID ADL35983 standard; protein; 336 AA.
DE Human NOVX polypeptide #14.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 39.4%; Score 712; DB 7; Length 336;
Best Local Similarity 50.2%; Pred. No. 9.7e-53;
RESULT 638
ID ADH71392 standard; protein; 253 AA.
DE Human protein of the invention NOV1ld SEQ ID NO:288.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.1%; Score 687.5; DB 8; Length 253;
Best Local Similarity 55.6%; Pred. No. 8.5e-51;
RESULT 639
ID AAU84385 standard; protein; 351 AA.
DE Novel human secreted or membrane-associated protein #24.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.

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PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 307;
Query Match Similarity 52.5%; Pred. No. 5.1e-57;
RESULT 610
ID ADH71410 standard; protein; 309 AA.
DE Human protein of the invention NOV11m SEQ ID NO:306.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 309;
Query Match Similarity 52.5%; Pred. No. 5.1e-57;
RESULT 611
ID ADH71406 standard; protein; 309 AA.
DE Human protein of the invention NOV11k SEQ ID NO:302.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 309;
Query Match Similarity 52.5%; Pred. No. 5.1e-57;
RESULT 612
ID AAE30253 standard; protein; 314 AA.
DE Human LP289 mature protein #2.
FN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI. 42.1%; Score 761; DB 6; Length 314;
Query Match Similarity 52.5%; Pred. No. 5.3e-57;
RESULT 613
ID ADH71394 standard; protein; 315 AA.
DE Human protein of the invention NOV11e SEQ ID NO:290.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 315;
Query Match Similarity 52.5%; Pred. No. 5.3e-57;
RESULT 614
ID ABG94637 standard; protein; 319 AA.
DE Human NOV5b protein.
FN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 5; Length 319;
Query Match Similarity 52.5%; Pred. No. 5.4e-57;
RESULT 615
ID ABG94636 standard; protein; 319 AA.
DE Human NOV5a protein.
FN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 5; Length 319;
Query Match Similarity 52.5%; Pred. No. 5.4e-57;
RESULT 616
ID ADL35977 standard; protein; 319 AA.
DE Human NOVX polypeptide #11.
FN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY) MALYANKAR U M. 42.1%; Score 761; DB 8; Length 336;
Query Match Similarity 50.6%; Pred. No. 7e-57;
RESULT 623
ID ADH71386 standard; protein; 336 AA.
DE Human protein of the invention NOV11a SEQ ID NO:282.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 42.1%; Score 760; DB 8; Length 336;
Query Match Similarity 50.6%; Pred. No. 7e-57;
RESULT 624
ID ABG94638 standard; protein; 307 AA.
DE Human NOV5c protein.
FN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 5; Length 307;
Query Match Similarity 52.5%; Pred. No. 1.1e-56;

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DE Human NOVX polypeptide #12.
FN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY) MALYANKAR U M. 42.1%; Score 761; DB 7; Length 319;
Query Match Similarity 52.5%; Pred. No. 5.4e-57;
RESULT 618
ID ADH71400 standard; protein; 319 AA.
DE Human protein of the invention NOV11h SEQ ID NO:296.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 319;
Query Match Similarity 52.5%; Pred. No. 5.4e-57;
RESULT 619
ID ADH71396 standard; protein; 319 AA.
DE Human protein of the invention NOV11f SEQ ID NO:292.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 319;
Query Match Similarity 52.5%; Pred. No. 5.4e-57;
RESULT 620
ID ADH71416 standard; protein; 320 AA.
DE Human protein of the invention NOV11p SEQ ID NO:312.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 320;
Query Match Similarity 52.5%; Pred. No. 5.4e-57;
RESULT 621
ID ADH71398 standard; protein; 325 AA.
DE Human protein of the invention NOV11g SEQ ID NO:294.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 325;
Query Match Similarity 52.5%; Pred. No. 5.5e-57;
RESULT 622
ID ADH71422 standard; protein; 336 AA.
DE Human protein of the invention NOV11s SEQ ID NO:318.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 42.1%; Score 760; DB 8; Length 336;
Query Match Similarity 50.6%; Pred. No. 7e-57;
RESULT 623
ID ADH71386 standard; protein; 336 AA.
DE Human protein of the invention NOV11a SEQ ID NO:282.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 42.1%; Score 760; DB 8; Length 336;
Query Match Similarity 50.6%; Pred. No. 7e-57;
RESULT 624
ID ABG94638 standard; protein; 307 AA.
DE Human NOV5c protein.
FN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 5; Length 307;
Query Match Similarity 52.5%; Pred. No. 1.1e-56;

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DE Human secreted/transmembrane protein, PRO4993.
PN US2003215908-A1.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 592
ID ADG49537 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 593
ID ADG48913 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 594
ID ADG51409 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 595
ID ADG59353 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 596
ID ADG62809 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 597
ID ADM17611 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 598
ID ADL07445 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 599
ID AAW05167 standard; protein; 252 AA.
DE Human LAMP residues 46-294.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 44.1%; Score 796.5; DB 2; Length 252;
Best Local Similarity 56.9%; Pred. No. 3.4e-60;
RESULT 600
ID AAW05168 standard; protein; 252 AA.
DE Rat LAMP residues 46-294.

PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 44.0%; Score 795.5; DB 2; Length 252;
Best Local Similarity 56.9%; Pred. No. 4.1e-60;
RESULT 601
ID ABG96271 standard; protein; 336 AA.
DE Human immunoglobulin superfamily protein IGSFP-9.
PN WO200272794-A2.
PD 19-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 42.2%; Score 763; DB 5; Length 336;
Best Local Similarity 50.6%; Pred. No. 3.9e-57;
RESULT 602
ID AAE29924 standard; protein; 336 AA.
DE Human LP289 protein.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 42.2%; Score 763; DB 6; Length 336;
Best Local Similarity 50.6%; Pred. No. 3.9e-57;
RESULT 603
ID ADH71418 standard; protein; 336 AA.
DE Human protein of the invention NOV11q SEQ ID NO:314.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.2%; Score 763; DB 8; Length 336;
Best Local Similarity 50.6%; Pred. No. 3.9e-57;
RESULT 604
ID ADH71412 standard; protein; 336 AA.
DE Human protein of the invention NOV11n SEQ ID NO:308.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.2%; Score 763; DB 8; Length 336;
Best Local Similarity 50.6%; Pred. No. 3.9e-57;
RESULT 605
ID ADH71414 standard; protein; 336 AA.
DE Human protein of the invention NOV11o SEQ ID NO:310.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.2%; Score 763; DB 8; Length 336;
Best Local Similarity 50.6%; Pred. No. 3.9e-57;
RESULT 606
ID ADH71388 standard; protein; 344 AA.
DE Human protein of the invention NOV11b SEQ ID NO:284.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.2%; Score 763; DB 8; Length 344;
Best Local Similarity 50.6%; Pred. No. 4e-57;
RESULT 607
ID ADH71390 standard; protein; 325 AA.
DE Human protein of the invention NOV11c SEQ ID NO:286.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.2%; Score 762; DB 8; Length 325;
Best Local Similarity 50.5%; Pred. No. 4.5e-57;
RESULT 608
ID AAE30252 standard; protein; 306 AA.
DE Human LP289 mature protein #1.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 42.1%; Score 761; DB 6; Length 306;
Best Local Similarity 52.5%; Pred. No. 5.1e-57;
RESULT 609
ID ADH71402 standard; protein; 307 AA.
DE Human protein of the invention NOV11i SEQ ID NO:298.
PN WO2003102155-A2.

PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEM/) STEWART T A.
PA (TUNA/) TUNAS D. P M.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 574
ID ADF61687 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 575
ID ADF40379 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 576
ID ADF46175 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 577
ID ADF24571 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 578
ID ADF41003 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 579
ID ADF23947 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 580
ID ADF33930 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 581
ID ADF27397 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 582
ID ADF28033 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 583
ID ADF41627 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 584
ID ADF33306 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 585
ID ADF25672 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 586
ID ADF26773 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 587
ID ADF34562 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 588
ID ADF46799 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 589
ID ADF50785 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 590
ID ADF50161 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 591
ID ADF52033 standard; protein; 352 AA.


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RESULT 558
ID ADC41653 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 559
ID ADC67708 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 560
ID ADC26644 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 561
ID ADC42277 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 562
ID ADE49646 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 563
ID ADE35700 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 564
ID ADE16814 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 565
ID ADD73429 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 566
ID ADD72787 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 567
ID ADE17438 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 568
ID ADF47452 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 569
ID ADG53209 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 570
ID ADG60529 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 571
ID ADI61289 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 572
ID ADE48946 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 573
ID ADE90047 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
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PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 3; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 540
ID ABO25277 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 541
ID ABU72283 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 542
ID ABU09489 standard; protein; 352 AA.
DE Human secreted and transmembrane PRO polypeptide #39.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 543
ID ABU61161 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 544
ID ABU80430 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO4993.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 545
ID ADA25150 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 546
ID ABO19732 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 547
ID ADA12812 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO4993.
PN US2003052116-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 548
ID ABO19623 standard; protein; 352 AA.
DE Novel human secreted and transmembrane polypeptide #91.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match 45.1%; Score 815; DB 6; Length 352;

Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 549
ID ADB74118 standard; protein; 352 AA.
DE Human PRO polypeptide #91.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 550
ID ADB76834 standard; protein; 352 AA.
DE Human PRO polypeptide #91.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 551
ID ADC44260 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 552
ID ADC62020 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 553
ID ADC63984 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 554
ID ADC67084 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 555
ID ADC69208 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 556
ID ADC63268 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 557
ID ADC68333 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;

PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 522
ID ADG11911 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 523
ID ADF94468 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 524
ID ADG06564 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 525
ID ADH38908 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 526
ID ADG63659 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 527
ID ADG33998 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 528
ID ADI33468 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 529
ID ADH69562 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 530
ID ADI29723 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096961-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 531
ID ADM27120 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 532
ID ADK66478 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 533
ID ADS82050 standard; protein; 354 AA.
DE Human cancer-associated protein #5.
PN WO2004035789-A1.
PD 29-APR-2004.
PA (GLDS) LG LIFE SCI LTD.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 534
ID ABB98407 standard; protein; 354 AA.
DE Human NOV6, KILON-like protein.
PN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.5%; Score 822; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 535
ID ADB64811 standard; protein; 354 AA.
DE Human protein encoded by clone OCBF20110210.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 45.4%; Score 820; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 5e-62;
RESULT 536
ID ABP53581 standard; protein; 354 AA.
DE Human NOV12b protein SEQ ID NO:26.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.3%; Score 819; DB 5; Length 354;
Best Local Similarity 48.6%; Pred. No. 6.1e-62;
RESULT 537
ID ABJ20234 standard; protein; 348 AA.
DE Human IG gene related protein SEQ ID NO:57.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 45.1%; Score 815; DB 6; Length 348;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 538
ID ABJ20233 standard; protein; 348 AA.
DE Human IG gene related protein SEQ ID NO:56.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 45.1%; Score 815; DB 6; Length 348;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 539
ID AAB44331 standard; protein; 352 AA.
DE Human PRO4993 protein sequence SEQ ID NO:612.
PN WO200053756-A2.
PD 14-SEP-2000.

DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 504
ID ADE04982 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 505
ID ADD75195 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 506
ID ADD76739 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 507
ID ADD86507 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 508
ID ADE41225 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 509
ID ADD77975 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 510
ID ADD77483 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 511
ID ADD77729 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 512
ID ADD85187 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.

PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 513
ID ADD73719 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 514
ID ADD74457 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 515
ID ADD76985 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 516
ID ADD85679 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 517
ID ADE05228 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 518
ID ADD74703 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 519
ID ADE05515 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 520
ID ADG27069 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 521
ID ADG11132 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096967-A1.

RESULT 485
ID ADE20876 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 486
ID ADE05720 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 487
ID ADD74949 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 488
ID ADD75695 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 489
ID ADD84927 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 490
ID ADD86753 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 491
ID ADE20630 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 492
ID ADE38927 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 493
ID ADE05474 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 494

ID ADD73459 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 495
ID ADD78299 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 496
ID ADE21122 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 497
ID ADD77237 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 498
ID ADE20384 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 499
ID ADD75449 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 500
ID ADD73965 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 501
ID ADD74211 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 502
ID ADD75941 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 503
ID ADD85433 standard; protein; 354 AA.

Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 467
ID ADB72893 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 468
ID ADC36731 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US200308065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 469
ID ADC21721 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 470
ID ADC49752 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US200308064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 471
ID ADC48951 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US200308070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 472
ID ADC49468 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US200308071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 473
ID ADC47329 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US200308072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 474
ID ADC47074 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 475
ID ADC77949 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;

Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 476
ID ADD06184 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 477
ID ADC77703 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US200308066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 478
ID ADD50666 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 479
ID ADD50912 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 480
ID ADD50393 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 481
ID ADD50147 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 482
ID ADD51158 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 483
ID ADG63811 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 484
ID ADC48705 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;

PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 449
ID ABU67170 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 450
ID ABU92048 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 451
ID ABU79812 standard; protein; 354 AA.
DE Human secreted/transmembrane protein PRO6004.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 452
ID ABJ72228 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 453
ID ADA47302 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 454
ID ABJ72356 standard; protein; 354 AA.
DE Human PRO6004 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 455
ID ABO34251 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO 6004.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 456
ID ABO19870 standard; protein; 354 AA.
DE Human secreted/transmembrane protein PRO6004.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 457
ID ABJ72058 standard; protein; 354 AA.
DE Human membrane bound receptor/protein PRO6004 amino acid sequence.
PN US2003085147-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 458
ID ADB83492 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 459
ID ADB80598 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 460
ID ADB73139 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 461
ID ADB78221 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 462
ID ADB84869 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 463
ID ADB77975 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 464
ID ADB87041 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 465
ID ADB84623 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 466
ID ADB83738 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

DE Rat LAMP clone 6c.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 50.6%; Score 913; DB 2; Length 361;
Best Local Similarity 51.7%; Pred. No. 4.9e-70;
RESULT 431
ID AAW05157 standard; protein; 308 AA.
DE Human LAMP residues 8-315.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 50.3%; Score 908; DB 2; Length 308;
Best Local Similarity 56.3%; Pred. No. 1.1e-69;
RESULT 432
ID AAW05158 standard; protein; 315 AA.
DE Rat LAMP residues 1-315.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 50.2%; Score 907; DB 2; Length 315;
Best Local Similarity 56.3%; Pred. No. 1.3e-69;
RESULT 433
ID AAW05156 standard; protein; 310 AA.
DE Rat mature LAMP.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 50.1%; Score 905; DB 2; Length 310;
Best Local Similarity 55.3%; Pred. No. 2e-69;
RESULT 434
ID AAW05155 standard; protein; 304 AA.
DE Human mature LAMP.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 49.9%; Score 902; DB 2; Length 304;
Best Local Similarity 55.5%; Pred. No. 3.5e-69;
RESULT 435
ID ABR39441 standard; protein; 383 AA.
DE Human GENSET polypeptide clone name SLAMP.
PN WO2003014151-A2.
PD 20-FEB-2003.
PA (GSEST) GENSET SA.
Query Match 49.4%; Score 893; DB 6; Length 383;
Best Local Similarity 53.3%; Pred. No. 2.8e-68;
RESULT 436
ID AAW05159 standard; protein; 287 AA.
DE Human LAMP residues 29-315.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 49.1%; Score 886.5; DB 2; Length 287;
Best Local Similarity 56.6%; Pred. No. 6.9e-68;
RESULT 437
ID AAW05160 standard; protein; 287 AA.
DE Rat LAMP residues 29-315.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 49.0%; Score 885.5; DB 2; Length 287;
Best Local Similarity 56.6%; Pred. No. 8.5e-68;
RESULT 438
ID ADM47275 standard; protein; 203 AA.
DE Oestrogen regulated protein like NOVX 25b protein.
PN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 48.4%; Score 873.5; DB 7; Length 203;
Best Local Similarity 54.5%; Pred. No. 5.7e-67;
RESULT 439
ID AAG75020 standard; protein; 326 AA.
DE Human colon cancer antigen protein SEQ ID NO:5784.

PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 47.2%; Score 852.5; DB 4; Length 326;
Best Local Similarity 51.6%; Pred. No. 7.1e-65;
RESULT 440
ID AAB31212 standard; protein; 354 AA.
DE Amino acid sequence of human polypeptide PRO6004.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 4; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 441
ID ABP53580 standard; protein; 354 AA.
DE Human NOV12a protein SEQ ID NO:24.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.6%; Score 823; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 442
ID AAU83592 standard; protein; 354 AA.
DE Human PRO protein, Seq ID No 2.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 443
ID ADI28023 standard; protein; 354 AA.
DE ECMCAD protein 708/904CD1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 45.6%; Score 823; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 444
ID ABU80739 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 445
ID ABO25183 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 446
ID ABO33705 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 447
ID ABU67301 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 448
ID ABU72069 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2002177165-A1.

DE Human neurotrophin.
PN US2003100485-A1.
PD 29-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 91.4%; Score 1650; DB 7; Length 355;
Best Local Similarity 92.2%; Pred. No. 1.3e-133;
RESULT 413
ID ADG63213 standard; protein; 367 AA.
DE Human neurotrophin protein +69bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 91.0%; Score 1644; DB 7; Length 367;
Best Local Similarity 89.1%; Pred. No. 4.5e-133;
RESULT 414
ID AAU79205 standard; protein; 381 AA.
DE Human Kruppel associated DNA binding protein 42.
PN WO200183541-A1.
PD 08-NOV-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 91.0%; Score 1643; DB 5; Length 381;
Best Local Similarity 98.7%; Pred. No. 5.7e-133;
RESULT 415
ID AAY57602 standard; protein; 313 AA.
DE Human protein SEQ ID NO:4.
PN WO9958668-A1.
PD 18-NOV-1999.
PA (ONCY) ONO PHARM CO LTD.
Query Match 90.9%; Score 1642; DB 3; Length 313;
Best Local Similarity 100.0%; Pred. No. 5.3e-133;
RESULT 416
ID ADI35772 standard; protein; 344 AA.
DE Rat neurotrophin.
PN US2003100485-A1.
PD 29-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 90.8%; Score 1639.5; DB 7; Length 344;
Best Local Similarity 92.9%; Pred. No. 1e-132;
RESULT 417
ID ADG63215 standard; protein; 376 AA.
DE Human neurotrophin protein +108bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 90.8%; Score 1639.5; DB 7; Length 376;
Best Local Similarity 87.0%; Pred. No. 1.1e-132;
RESULT 418
ID ADE07928 standard; protein; 338 AA.
DE Novel protein (useful for identifying genetic disorders) #83.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 71.7%; Score 1295.5; DB 7; Length 338;
Best Local Similarity 71.6%; Pred. No. 4.6e-103;
RESULT 419
ID ADO47380 standard; protein; 250 AA.
DE Human neurotrophin-like protein-related rat neurotrophin protein SeqID15.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 71.7%; Score 1295; DB 8; Length 250;
Best Local Similarity 97.6%; Pred. No. 3.3e-103;
RESULT 420
ID ABJ20236 standard; protein; 345 AA.
DE Human IG gene related protein SEQ ID No 59.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 70.2%; Score 1268; DB 6; Length 345;
Best Local Similarity 71.2%; Pred. No. 1.1e-100;
RESULT 421
ID ADE83448 standard; protein; 345 AA.
DE Human Protein Q14982, SEQ ID NO 11043.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 70.2%; Score 1268; DB 7; Length 345;
Best Local Similarity 71.2%; Pred. No. 1.1e-100;
RESULT 422
ID ADG63207 standard; protein; 345 AA.
DE Opioid-binding protein/cell adhesion molecule-like protein.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 70.2%; Score 1268; DB 7; Length 345;
Best Local Similarity 71.2%; Pred. No. 1.1e-100;
RESULT 423
ID ADE83446 standard; protein; 345 AA.
DE Rat Protein P32736, SEQ ID NO 11041.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 69.7%; Score 1259; DB 7; Length 345;
Best Local Similarity 71.2%; Pred. No. 6.6e-100;
RESULT 424
ID AAO19641 standard; protein; 335 AA.
DE Human limbic system associated membrane protein 36-85.
PN CN1345756-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 51.6%; Score 932.5; DB 5; Length 335;
Best Local Similarity 53.9%; Pred. No. 9.2e-72;
RESULT 425
ID ABJ20235 standard; protein; 338 AA.
DE Human IG gene related protein SEQ ID No 58.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 51.6%; Score 931.5; DB 6; Length 338;
Best Local Similarity 55.4%; Pred. No. 1.1e-71;
RESULT 426
ID ADL12675 standard; protein; 338 AA.
DE Human steroid-induced C3A liver cell protein #60.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 51.6%; Score 931.5; DB 8; Length 338;
Best Local Similarity 55.4%; Pred. No. 1.1e-71;
RESULT 427
ID AAW05153 standard; protein; 338 AA.
DE Rat LAMP residues 1-332.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.1e-71;
RESULT 428
ID AAW05154 standard; protein; 338 AA.
DE Rat LAMP residues 1-332.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.1e-71;
RESULT 429
ID AAW05152 standard; protein; 325 AA.
DE Human LAMP residues 8-332.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 51.1%; Score 923.5; DB 2; Length 325;
Best Local Similarity 55.3%; Pred. No. 5.3e-71;
RESULT 430
ID AAW05172 standard; protein; 361 AA.

RESULT 394
ID ADL07356 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GSETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 395
ID AD442464 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GSETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 396
ID ADM28326 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GSETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 397
ID AD195808 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GSETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 398
ID AD196360 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GSETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 399
ID AAM40499 standard; protein; 355 AA.
DE Human polypeptide SEQ ID NO 5430.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 4; Length 355;
RESULT 400
ID AD121580 standard; protein; 355 AA.
DE Novel human polypeptide #59.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 355;
RESULT 401
ID AAB19722 standard; protein; 344 AA.
DE Human SECX Clone 11753149.0.37-encoded protein.
PN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 99.6%; Score 1799; DB 3; Length 344;
RESULT 402
ID AAB19721 standard; protein; 344 AA.
DE Human SECX Clone 11753149.0.6-encoded protein.
PN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 99.6%; Score 1799; DB 3; Length 344;
RESULT 403
ID ADI35770 standard; protein; 355 AA.
DE Human neurotrophin protein.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match
Best Local Similarity 92.2%; Score 1665.5; DB 7; Length 344;
RESULT 404
ID AD18291 standard; protein; 344 AA.
DE Human molecule (MOL) protein MOL11.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 99.6%; Score 1799; DB 7; Length 344;
RESULT 405
ID AAY41773 standard; protein; 343 AA.
DE Human PRO337 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 99.7%; Score 1791.5; DB 2; Length 343;
RESULT 406
ID AAM38713 standard; protein; 344 AA.
DE Human polypeptide SEQ ID NO 1858.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 92.2%; Score 1665.5; DB 4; Length 344;
RESULT 407
ID ABJ20227 standard; protein; 344 AA.
DE Human IG gene related protein SEQ ID NO 50.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 95.2%; Score 1665.5; DB 6; Length 344;
RESULT 408
ID ABUS6719 standard; protein; 344 AA.
DE Lung cancer-associated polypeptide #312.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 92.2%; Score 1665.5; DB 6; Length 344;
RESULT 409
ID ADG63209 standard; protein; 344 AA.
DE Human neurotrophin protein.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match
Best Local Similarity 92.2%; Score 1665.5; DB 7; Length 344;
RESULT 410
ID ADN39338 standard; protein; 344 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:456.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 92.2%; Score 1665.5; DB 7; Length 344;
RESULT 411
ID ADG63211 standard; protein; 355 AA.
DE Human neurotrophin protein +33bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match
Best Local Similarity 91.4%; Score 1650; DB 7; Length 355;
RESULT 412
ID ADI35770 standard; protein; 355 AA.

Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 376
ID ADI18165 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 377
ID ADI33592 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 378
ID ADH69686 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 379
ID ADH25745 standard; protein; 344 AA.
DE Human PRO337 protein SEQ ID NO:523.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 380
ID ADG09908 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 381
ID ADI15379 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 382
ID ADG09256 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 383
ID ADI14711 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 384
ID ADI29847 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;

Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 385
ID ADI18306 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 386
ID ADM27244 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 387
ID ADJ63587 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 388
ID ADJ77482 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 389
ID ADK82834 standard; protein; 344 AA.
DE Human PRO polypeptide #28.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 390
ID ADK66602 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 391
ID ADJ65604 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 392
ID ADM27740 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 393
ID ADM17522 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 394
ID ADI29847 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 358
ID ADG50072 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein, PRO337.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 359
ID ADG51944 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 360
ID ADG52421 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 361
ID ADG54149 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 362
ID ADG49448 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 363
ID ADG81118 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 364
ID ADG56357 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 365
ID ADH12623 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 366
ID ADG48824 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003216560-A1.
PD 20-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 367
ID ADG61469 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 368
ID ADH28556 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003202331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 369
ID ADG54701 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 370
ID ADG59741 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 371
ID ADG51320 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 372
ID ADH43489 standard; protein; 344 AA.
DE Human PRO polypeptide #28.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 373
ID ADG59264 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 374
ID ADG34122 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 375
ID ADG62720 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.

ID ADG06688 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 340
ID ADG55253 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 341
ID ADG60917 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 342
ID ADG62021 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 343
ID ADG82222 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 344
ID ADG57461 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 345
ID ADG56909 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 346
ID ADG55805 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 347
ID ADG58565 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 348
ID ADG70931 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO337.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 349
ID ADH39032 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 350
ID ADG58013 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 351
ID ADG53597 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 352
ID ADG71483 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 353
ID ADG50696 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 354
ID ADG81670 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 355
ID ADH30632 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 356
ID ADG63634 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 357
ID ADH1999 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207419-A1.

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Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 321
ID ADG03456 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 322
ID ADF99177 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 323
ID ADG16762 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 324
ID ADG05221 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 325
ID ADG19488 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 326
ID ADG11256 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 327
ID ADG13325 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 328
ID ADG08382 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 329
ID ADG15552 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 330
ID ADG12035 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 331
ID ADF96950 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 332
ID ADG06135 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 333
ID ADG23719 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 334
ID ADG04008 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 335
ID ADG24909 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 336
ID ADF94592 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 337
ID ADG07206 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 338
ID ADG07758 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 339
ID ADG07758 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 303
ID ADF27944 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 304
ID ADE92265 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 305
ID ADE90566 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 306
ID ADF41538 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 307
ID ADF33217 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 308
ID ADF25583 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 309
ID ADF26684 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 310
ID ADF34473 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 311
ID ADF46710 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 312
ID ADE91713 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 313
ID ADG05639 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 314
ID ADG27193 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 315
ID ADG02292 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 316
ID ADG22078 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 317
ID ADG20148 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 318
ID ADF98054 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 319
ID ADG24271 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 320
ID ADF98625 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
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PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 295
ID ADD74581 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 286
ID AD077109 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 287
ID AD085803 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 288
ID ADE05352 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 289
ID AD074827 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 290
ID ADF61598 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 291
ID ADF40290 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 292
ID ADF46086 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 293
ID ADE94707 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199027-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 294
ID ADE91118 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 295
ID ADE95259 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 296
ID ADE93369 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 297
ID ADF24482 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 298
ID ADF40914 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 299
ID ADF23858 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 300
ID ADF33841 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 301
ID ADF34950 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 302
ID ADF27308 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199436-A1.
PD 23-OCT-2003.


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PD US2003092111-A1.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 270
ID ADD87373 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 271
ID ADE05106 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 272
ID ADD75319 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 273
ID ADD76863 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 274
ID ADD86631 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 275
ID ADE89239 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 276
ID ADE41199 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 277
ID ADD78099 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 278
ID ADE18378 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 279
ID ADE88687 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 280
ID ADE89958 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAFI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 281
ID ADD77607 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 282
ID ADD77853 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 283
ID ADD85311 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 284
ID ADD73843 standard; protein; 344 AA.
DE Human PRO polypeptide #63.

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ID ADD87925 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 252
ID ADD86329 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 253
ID ADE05598 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 254
ID ADD73583 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 255
ID ADE75777 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 256
ID ADE48857 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 257
ID ADD78423 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 258
ID ADE41306 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 259
ID ADE23353 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 260
ID ADE21246 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO337.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 261
ID ADD77361 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 262
ID ADE20508 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 263
ID ADD75573 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 264
ID ADD74089 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 265
ID ADD74335 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 266
ID ADD76065 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 267
ID ADD85557 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 268
ID ADE23905 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 269
ID ADE24548 standard; protein; 344 AA.
DE Human PRO polypeptide #188.

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Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 233
ID ADH81939 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100735-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 234
ID ADH81387 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 235
ID ADM82556 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 236
ID ADN15955 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 237
ID ADN16584 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 238
ID ADN15403 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 239
ID ADN14851 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 240
ID ADC48829 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 241
ID ADC81113 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 242
ID ADE21000 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 243
ID ADE05844 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 244
ID ADD76561 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 245
ID ADD75073 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 246
ID ADD75819 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 247
ID ADD85051 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 248
ID ADD86877 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 249
ID ADE20754 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 250
ID ADE39051 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US200309362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 251
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 215
ID ADG40889 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 216
ID ADR04688 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 217
ID ADE92817 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 218
ID ADF47363 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 219
ID ADG21526 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 220
ID ADG23167 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 221
ID ADF97502 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 222
ID ADG80566 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 223
ID ADE53120 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 224
ID ADG60440 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 225
ID ADG80014 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 226
ID ADG63785 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 227
ID ADH55306 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 228
ID ADH55858 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 229
ID ADI61200 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 230
ID ADI64077 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 231
ID ADI65026 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 232
ID ADI63525 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 233
ID ADI63525 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;

PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 197
ID ADE17826 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 198
ID ADD91958 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 199
ID ADE33421 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 200
ID ADE33973 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 201
ID ADD80025 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 202
ID ADD93062 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 203
ID ADD72698 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 204
ID ADE19482 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 205
ID ADE18930 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199026-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 206
ID ADE43126 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 207
ID ADD95915 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 208
ID ADE22801 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 209
ID ADD78919 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 210
ID ADE32869 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 211
ID ADE42561 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 212
ID ADE17349 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 213
ID ADD80577 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 214
ID ADD89605 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199028-A1.
PD 23-OCT-2003.

ID ADD37098 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 179
ID ADD51778 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 180
ID ADD02577 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 181
ID ADD50517 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 182
ID ADD02011 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 183
ID ADD54193 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 184
ID ADD50271 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 185
ID ADD51282 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 186
ID ADA49557 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 187
ID ADD92510 standard; protein; 344 AA.

DE Human PRO polypeptide #188.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 188
ID ADD91406 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 189
ID ADE04020 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 190
ID ADE32317 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 191
ID ADE22249 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 192
ID ADD79473 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 193
ID ADE35611 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 194
ID ADE16725 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 195
ID ADD73340 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 196
ID ADA42009 standard; protein; 344 AA.
DE Human PRO polypeptide #188.

Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 160
ID ADC80009 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 161
ID ADC78073 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 162
ID ADD04605 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 163
ID ADD06308 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 164
ID ADC80561 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 165
ID ADD1068 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 166
ID ADD10345 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 167
ID ADC47949 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 168
ID ADC77827 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 169
ID ADC80009 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 170
ID ADD11305 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 171
ID ADD09478 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 172
ID ADD50790 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 173
ID ADD41191 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 174
ID ADD52330 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 175
ID ADD51036 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 176
ID ADD53070 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 177
ID ADD53622 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 178

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 142
ID ADC49075 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 143
ID ADC49592 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 144
ID ADC47453 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 145
ID ADC52950 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 146
ID ADC57304 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 147
ID ADC60495 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 148
ID ADC50970 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 149
ID ADC65497 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 150
ID ADC54595 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 151
ID ADC53556 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 152
ID ADC59079 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 153
ID ADC5957 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 154
ID ADC58527 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 155
ID ADC47198 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 156
ID ADD03201 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 157
ID ADC90193 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 158
ID ADC69612 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 159
ID ADC48501 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 160
ID ADC48501 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;

PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 124
ID ADB46544 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 125
ID ADC44171 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 126
ID ADC61931 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003049694-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 127
ID ADC63895 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 128
ID ADC66995 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 129
ID ADC69119 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 130
ID ADC63179 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 131
ID ADC68244 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 132
ID ADC41564 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003072745-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 133
ID ADC67619 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 134
ID ADC62555 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 135
ID ADC36855 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 136
ID ADC42188 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 137
ID ADC21845 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 138
ID ADC50417 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 139
ID ADC71964 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 140
ID ADC59943 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 141
ID ADC49876 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088064-A1.
PD 08-MAY-2003.

ID ADB84993 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 106
ID ADB89668 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 107
ID ADB90400 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 108
ID ADB39501 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 109
ID ADB78099 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 110
ID ADB74029 standard; protein; 344 AA.
DE Human PRO polypeptide #89.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 111
ID ADB87165 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US200308067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 112
ID ADB84747 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 113
ID ADB47124 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 114
ID ADB83862 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO337.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 115
ID ADB86731 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 116
ID ADB73017 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 117
ID ADB76745 standard; protein; 344 AA.
DE Human PRO polypeptide #89.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 118
ID ADB77336 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 119
ID ADB34493 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 120
ID ADB35597 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 121
ID ADB33941 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 122
ID ADB35045 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 123
ID ADB36149 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 87
ID ADA98611 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 88
ID ADA97616 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 89
ID ADB27373 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 90
ID ADB22306 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 91
ID ABO19862 standard; protein; 344 AA.
DE Human secreted/transmembrane protein PRO337.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 92
ID ABJ72120 standard; protein; 344 AA.
DE Human membrane bound receptor/protein PRO337 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 93
ID ADA66997 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 94
ID ADB22858 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 95
ID ADB23631 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;

RESULT 96
ID ADA92353 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 97
ID ADB15416 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 98
ID ADB83616 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 99
ID ADB80722 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 100
ID ADB73263 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096368-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 101
ID ADB38668 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 102
ID ADB78345 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 103
ID ADB38116 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 104
ID ADB66588 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 105
ID ADB66588 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;

DE Human PRO polypeptide #188.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 69
ID ABO19621 standard; protein; 344 AA.
DE Human PRO337 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 70
ID ADA61036 standard; protein; 344 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 71
ID ADB24183 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 72
ID ADA96512 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 73
ID ADA81084 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 74
ID ADA95960 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 75
ID ADB26269 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 76
ID ADB21754 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 77
ID ABO34313 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO 337.
PN US2003059909-A1.
PD 27-MAR-2003.

PN US200304934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 78
ID ABO19621 standard; protein; 344 AA.
DE Novel human secreted and transmembrane polypeptide #89.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 79
ID ADA77533 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 80
ID ADB18273 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 81
ID ADA86956 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 82
ID ADA88059 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 83
ID ADA6447 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 84
ID ADB28477 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 85
ID ADB29029 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 86
ID ADA76981 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003059909-A1.
PD 27-MAR-2003.

RESULT 50
ID ADB19936 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 51
ID ADB13248 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 52
ID ABO4336 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 53
ID ABO19730 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 54
ID ADA12723 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003052216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 55
ID ADA4502 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 56
ID ADB24735 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077113-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 57
ID ADA82259 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 58
ID ADA5222 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 59

ID ADA85300 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 60
ID ADA84748 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 61
ID ADB30004 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 62
ID ADA80532 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 63
ID ADA75774 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 64
ID ADA46999 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 65
ID ADB25295 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077115-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 66
ID ADA93471 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 67
ID ADB26821 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 68
ID ADB31108 standard; protein; 344 AA.

Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 32
 ID ADB19384 standard; protein; 344 AA.
 DE Human PRO polypeptide and transmembrane protein PRO337.
 PN US2003068796-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 33
 ID ADB27925 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003082704-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 34
 ID ADA86404 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003082711-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 35
 ID ADB1968 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003087350-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 36
 ID ADA47754 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003073215-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 37
 ID ADA67549 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003068795-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 38
 ID ADB30556 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003068794-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 39
 ID ADA85852 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003082693-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 40
 ID ADA97064 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003082705-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;

Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 41
 ID ADA79368 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003082763-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 42
 ID ADA87507 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003087345-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 43
 ID ADB16709 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003087349-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 44
 ID ADA91801 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003082694-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 45
 ID ADB14864 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003087351-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 46
 ID ADA25062 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003050241-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 47
 ID ADA47276 standard; protein; 344 AA.
 DE Human secreted/transmembrane polypeptide PRO337.
 PN US2003044844-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 48
 ID ADB18825 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003073211-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 49
 ID ADA94040 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003077722-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;

PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 14
ID ABU72281 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 15
ID ABU66757 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 16
ID ABU67293 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 17
ID ABU67293 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 18
ID ABU59838 standard; protein; 344 AA.
DE Novel secreted and transmembrane protein PRO337.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 19
ID ABU61159 standard; protein; 344 AA.
DE Human PRO337 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 20
ID ABO25028 standard; protein; 344 AA.
DE Human secreted/transmembrane protein (PRO) #188.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 21
ID ABU72061 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US200217165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 22
ID ABU67162 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003032062-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 23
ID ABU80428 standard; protein; 344 AA.
DE Human secreted/transmembrane protein PRO337.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 24
ID ABU82110 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US200308063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 25
ID ABU67033 standard; protein; 344 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 376.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 26
ID ABU79804 standard; protein; 344 AA.
DE Human secreted/transmembrane protein PRO337.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 27
ID ADA45895 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 28
ID ADA76326 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 29
ID ABU72290 standard; protein; 344 AA.
DE Human PRO337 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 30
ID ADA18976 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 31
ID ADA61599 standard; protein; 344 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

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GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: June 3, 2005, 14:09:27 ; Search time 73 Seconds
        (without alignments)
        1822.542 Million cell updates/sec

US-09-978-544a-523
Title:
Perfect score: 1806
Sequence: 1 MKTIQPMWHSISWAIPTGL.....RRAGCVLLPLVLHLLKF 344
Scoring table: BLOSUM62

Searched:
Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database :
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES

No. Score Match Length DB ID Description
RESULT 1
ID AAY57601 standard; protein; 344 AA.
DE Human protein SEQ ID NO:1.
PN WO958668-A1.
PD 18-NOV-1999.
PA (ONOV) ONO PHARM CO LTD.
Query Match 100.0%; Score 1806; DB 3; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 2
ID AAB44329 standard; protein; 344 AA.
DE Human PRO337 protein sequence SEQ ID NO:523.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 3; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 3
ID AAB31204 standard; protein; 344 AA.
DE Amino acid sequence of human polypeptide PRO337.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 4
ID AAU12359 standard; protein; 344 AA.
DE Human PRO337 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 5
ID AAU83654 standard; protein; 344 AA.
DE Human PRO protein, Seq ID NO 126.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 6
ID ABB84844 standard; protein; 344 AA.
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DE Human PRO337 protein sequence SEQ ID NO:56.
PN WO20020690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 7
ID ABB95450 standard; protein; 344 AA.
DE Human angiogenesis related protein PRO337 SEQ ID NO: 56.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 8
ID ABO17803 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 9
ID ABU80801 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 10
ID ABO25175 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 11
ID ABO25275 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 12
ID ABO33767 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 13
ID ABU81057 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003004311-A1.
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